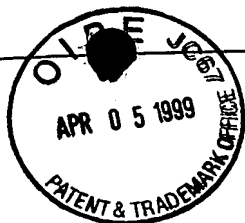


HT, 0560



1

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- A'
- (i) APPLICANT: Malcolm, Bruce  
Taremi, Shahriar S.  
Weber, Patricia  
Yao, Nanhua
  - (ii) TITLE OF INVENTION: Covalent Complexes of Hepatitis C Virus  
NS3 Protease and NS4A Cofactor Peptide
  - (iii) NUMBER OF SEQUENCES: 123
  - (iv) CORRESPONDENCE ADDRESS:
    - (A) ADDRESSEE: Schering-Plough Corp.
    - (B) STREET: 2000 Galloping Hill Road
    - (C) CITY: Kenilworth
    - (D) STATE: New Jersey
    - (E) COUNTRY: USA
    - (F) ZIP: 07030
  - (v) COMPUTER READABLE FORM:
    - (A) MEDIUM TYPE: Floppy disk
    - (B) COMPUTER: Power Macintosh
    - (C) OPERATING SYSTEM: 8.0.1
    - (D) SOFTWARE: Microsoft Word 6.0.1
  - (vi) CURRENT APPLICATION DATA:
    - (A) APPLICATION NUMBER: US 09/198,723
    - (B) FILING DATE: 24 NOV 1998
    - (C) CLASSIFICATION:
  - (viii) ATTORNEY/AGENT INFORMATION:
    - (A) NAME: McLaughlin, Jaye P.
    - (B) REGISTRATION NUMBER: 41,211
    - (C) REFERENCE/DOCKET NUMBER: JB0800
  - (ix) TELECOMMUNICATION INFORMATION:
    - (A) TELEPHONE: (908)298-5056
    - (B) TELEFAX: (908)298-5388

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 216 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro

56

1	5	10	15
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	20	25	30
Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu	35	40	45
Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val	50	55	60
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala	65	70	75
Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser	85	90	95
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn	100	105	110
Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser	115	120	125
Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg	130	135	140
His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser	145	150	155
Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly	165	170	175
Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala	180	185	190
Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu	195	200	205
Ser Met Glu Thr Thr Met Arg Ser	210	215	

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro	1	5	10	15
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu				

20	25	30
Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu		
35	40	45
Leu Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val		
50	55	60
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala		
65	70	75
Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser		
85	90	95
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn		
100	105	110
Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser		
115	120	125
Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg		
130	135	140
His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser		
145	150	155
Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly		
165	170	175
Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala		
180	185	190
Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu		
195	200	205
Ser Met Glu Thr Thr Met Arg Ser		
210	215	

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro		
1	5	10
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu		
20	25	30
Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu		

58

35	40	45
Leu Gly Cys Ile Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val		
50	55	60
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala		
65	70	75
Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser		
	85	90
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn		
	100	105
Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser		
	115	120
Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg		
	130	135
His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser		
	145	150
Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly		
	165	170
Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala		
	180	185
Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu		
	195	200
Ser Met Glu Thr Thr Met Arg Ser		
	210	215

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro		
1	5	10
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu		
	20	25
Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu		
	35	40
Leu Gly Cys Lys Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val		
		45

50		55		60
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala	65	70	75	80
Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser		85	90	95
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn	100		105	110
Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser	115	120		125
Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg	130	135	140	
His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser	145	150	155	160
Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly		165	170	175
Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala	180	185		190
Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu	195	200	205	
Ser Met Glu Thr Thr Met Arg Ser	210	215		

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro	1	5	10	15
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	20	25	30	
Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu	35	40	45	
Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val	50	55	60	
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala				

65		70		75		80									
Thr	Cys	Val	Asn	Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser
				85					90					95	
Lys	Thr	Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn
			100					105					110		
Val	Asp	Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser
		115					120					125			
Leu	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg
	130					135					140				
His	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser
145					150					155					160
Leu	Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ala	Gly	Gly
				165					170					175	
Pro	Leu	Leu	Cys	Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala
			180					185					190		
Val	Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu
	195						200					205			
Ser	Met	Glu	Thr	Thr	Met	Arg	Ser								
	210					215									

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Gly	Ser	Ser	His	His	His	His	His	His	Ser	Ser	Gly	Leu	Val	Pro
1				5					10					15	
Arg	Gly	Ser	His	Met	Gly	Ser	Val	Val	Ile	Val	Gly	Arg	Ile	Ile	Leu
			20					25					30		
Ser	Gly	Ser	Gly	Ser	Ile	Thr	Ala	Tyr	Ser	Gln	Gln	Thr	Arg	Gly	Leu
		35					40					45			
Leu	Gly	Cys	Lys	Ile	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val
	50					55					60				
Glu	Gly	Glu	Val	Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala
	65				70					75					80
Thr	Cys	Val	Asn	Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser

lec

Lys	Thr	Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn
			100						105					110	
Val	Asp	Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser
		115					120					125			
Leu	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg
	130					135					140				
His	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser
145					150					155					160
Leu	Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ala	Gly	Gly
				165					170					175	
Pro	Leu	Leu	Cys	Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala
			180					185					190		
Val	Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu
		195					200					205			
Ser	Met	Glu	Thr	Thr	Met	Arg	Ser								
	210						215								

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Gly	Ser	Ser	His	His	His	His	His	His	Ser	Ser	Gly	Leu	Val	Pro
1				5					10					15	
Arg	Gly	Ser	His	Met	Gly	Ser	Val	Val	Ile	Val	Gly	Arg	Ile	Ile	Leu
			20					25					30		
Ser	Gly	Ser	Gly	Ser	Ile	Thr	Ala	Tyr	Ser	Gln	Gln	Thr	Arg	Gly	Leu
		35					40					45			
Leu	Gly	Cys	Ile	Lys	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val
	50					55					60				
Glu	Gly	Glu	Val	Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala
65					70					75					80
Thr	Cys	Val	Asn	Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser
				85					90					95	
Lys	Thr	Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn

6

100	105	110
Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser		
115	120	125
Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg		
130	135	140
His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser		
145	150	155
Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly		
	165	170
Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala		
	180	185
Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu		
195	200	205
Ser Met Glu Thr Thr Met Arg Ser		
210	215	

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro		
1	5	10
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu		
	20	25
Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu		
35	40	45
Leu Gly Cys Lys Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val		
50	55	60
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala		
65	70	75
Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser		
	85	90
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn		
100	105	110
Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser		



115	120	125
Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg		
130	135	140
His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser		
145	150	155 160
Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly		
	165	170 175
Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala		
	180	185 190
Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu		
	195	200 205
Ser Met Glu Thr Thr Met Arg Ser		
210	215	

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 216 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro		
1	5	10 15
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu		
	20	25 30
Ser Pro Ala Gly Gly Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu		
	35	40 45
Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val		
	50	55 60
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala		
	65	70 75 80
Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser		
	85	90 95
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn		
	100	105 110
Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser		
	115	120 125

Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg  
 130 135 140  
 His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser  
 145 150 155 160  
 Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly  
 165 170 175  
 Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala  
 180 185 190  
 Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu  
 195 200 205  
 Ser Met Glu Thr Thr Met Arg Ser  
 210 215

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro  
 1 5 10 15  
 Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu  
 20 25 30  
 Ser Pro Ala Gly Gly Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu  
 35 40 45  
 Leu Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val  
 50 55 60  
 Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala  
 65 70 75 80  
 Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser  
 85 90 95  
 Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn  
 100 105 110  
 Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser  
 115 120 125  
 Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg  
 130 135 140

His	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	145	150	155	160
Leu	Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly	165	170	175	
Pro	Leu	Leu	Cys	Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	180	185	190	
Val	Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	195	200	205	
Ser	Met	Glu	Thr	Thr	Met	Arg	Ser									210	215		

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Gly	Ser	Ser	His	His	His	His	His	His	Ser	Ser	Gly	Leu	Val	Pro	1	5	10	15
Arg	Gly	Ser	His	Met	Gly	Ser	Val	Val	Ile	Val	Gly	Arg	Ile	Ile	Leu	20	25	30	
Ser	Gly	Ser	Gly	Ser	Ile	Thr	Ala	Tyr	Ser	Gln	Gln	Thr	Arg	Gly	Leu	35	40	45	
Leu	Gly	Cys	Ile	Ile	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val	50	55	60	
Glu	Gly	Glu	Val	Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala	65	70	75	80
Thr	Cys	Val	Asn	Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser	85	90	95	
Lys	Thr	Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	100	105	110	
Val	Asp	Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	115	120	125	
Leu	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	130	135	140	
His	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	145	150	155	160

Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly  
 165 170 175  
 Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala  
 180 185 190  
 Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu  
 195 200 205  
 Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser  
 210 215 220  
 Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro  
 225 230 235 240  
 Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln  
 245 250 255  
 Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly  
 260 265 270  
 Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg  
 275 280 285  
 Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr  
 290 295 300  
 Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp  
 305 310 315 320  
 Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu  
 325 330 335  
 Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu  
 340 345 350  
 Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His  
 355 360 365  
 Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe  
 370 375 380  
 Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu  
 385 390 395 400  
 Ile Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu  
 405 410 415  
 Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val  
 420 425 430  
 Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala  
 435 440 445  
 Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn  
 450 455 460  
 Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr

465		470		475		480
Ile Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg						
		485		490		495
Arg Gly Arg Thr Gly Arg Gly Arg Arg Gly Ile Tyr Arg Phe Val Thr						
		500		505		510
Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu						
		515		520		525
Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr						
		530		535		540
Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys						
		545		550		555
Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His						
		565		570		575
Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe						
		580		585		590
Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala						
		595		600		605
Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys						
		610		615		620
Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val						
		625		630		635
Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala						
		645		650		655
Cys Met Ser Ala Asp Leu Glu Val Val Thr						
		660		665		

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro														
1				5					10				15	
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu														
				20				25				30		
Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu														

35	40	45
Leu Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val		
50	55	60
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala		
65	70	75
Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser		
	85	90
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn		
	100	105
Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser		
	115	120
Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg		
	130	135
His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser		
145	150	155
Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly		
	165	170
Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala		
	180	185
Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu		
	195	200
Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser		
	210	215
Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro		
225	230	235
Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln		
	245	250
Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly		
	260	265
Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg		
	275	280
Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr		
	290	295
Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp		
305	310	315
Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu		
	325	330
Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu		
	340	345
		350

Val	Val	Leu	Ala	Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Val	Pro	His	355	360	365	
Pro	Asn	Ile	Glu	Glu	Val	Ala	Leu	Ser	Asn	Thr	Gly	Glu	Ile	Pro	Phe	370	375	380	
Tyr	Gly	Lys	Ala	Ile	Pro	Ile	Glu	Ala	Ile	Arg	Gly	Gly	Arg	His	Leu	385	390	395	400
Ile	Phe	Cys	His	Ser	Lys	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Ala	Lys	Leu	405	410	415	
Ser	Gly	Leu	Gly	Ile	Asn	Ala	Val	Ala	Tyr	Tyr	Arg	Gly	Leu	Asp	Val	420	425	430	
Ser	Val	Ile	Pro	Thr	Ile	Gly	Asp	Val	Val	Val	Val	Ala	Thr	Asp	Ala	435	440	445	
Leu	Met	Thr	Gly	Tyr	Thr	Gly	Asp	Phe	Asp	Ser	Val	Ile	Asp	Cys	Asn	450	455	460	
Thr	Cys	Val	Thr	Gln	Thr	Val	Asp	Phe	Ser	Leu	Asp	Pro	Thr	Phe	Thr	465	470	475	480
Ile	Glu	Thr	Thr	Thr	Val	Pro	Gln	Asp	Ala	Val	Ser	Arg	Ser	Gln	Arg	485	490	495	
Arg	Gly	Arg	Thr	Gly	Arg	Gly	Arg	Arg	Gly	Ile	Tyr	Arg	Phe	Val	Thr	500	505	510	
Pro	Gly	Glu	Arg	Pro	Ser	Gly	Met	Phe	Asp	Ser	Ser	Val	Leu	Cys	Glu	515	520	525	
Cys	Tyr	Asp	Ala	Gly	Cys	Ala	Trp	Tyr	Glu	Leu	Thr	Pro	Ala	Glu	Thr	530	535	540	
Ser	Val	Arg	Leu	Arg	Ala	Tyr	Leu	Asn	Thr	Pro	Gly	Leu	Pro	Val	Cys	545	550	555	560
Gln	Asp	His	Leu	Glu	Phe	Trp	Glu	Ser	Val	Phe	Thr	Gly	Leu	Thr	His	565	570	575	
Ile	Asp	Ala	His	Phe	Leu	Ser	Gln	Thr	Lys	Gln	Ala	Gly	Asp	Asn	Phe	580	585	590	
Pro	Tyr	Leu	Val	Ala	Tyr	Gln	Ala	Thr	Val	Cys	Ala	Arg	Ala	Gln	Ala	595	600	605	
Pro	Pro	Pro	Ser	Trp	Asp	Gln	Met	Trp	Lys	Cys	Leu	Ile	Arg	Leu	Lys	610	615	620	
Pro	Thr	Leu	His	Gly	Pro	Thr	Pro	Leu	Leu	Tyr	Arg	Leu	Gly	Ala	Val	625	630	635	640
Gln	Asn	Glu	Val	Thr	Leu	Thr	His	Pro	Ile	Thr	Lys	Tyr	Ile	Met	Ala	645	650	655	

Cys Met Ser Ala Asp Leu Glu Val Val Thr  
 660 665

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 666 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Gly	Ser	Ser	His	His	His	His	His	His	Ser	Ser	Gly	Leu	Val	Pro	1	5	10	15
Arg	Gly	Ser	His	Met	Gly	Ser	Val	Val	Ile	Val	Gly	Arg	Ile	Ile	Leu	20	25	30	
Ser	Gly	Ser	Gly	Ser	Ile	Thr	Ala	Tyr	Ser	Gln	Gln	Thr	Arg	Gly	Leu	35	40	45	
Leu	Gly	Cys	Ile	Lys	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val	50	55	60	
Glu	Gly	Glu	Val	Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala	65	70	75	80
Thr	Cys	Val	Asn	Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser	85	90	95	
Lys	Thr	Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	100	105	110	
Val	Asp	Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	115	120	125	
Leu	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	130	135	140	
His	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	145	150	155	160
Leu	Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly	165	170	175	
Pro	Leu	Leu	Cys	Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	180	185	190	
Val	Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	195	200	205	
Ser	Met	Glu	Thr	Thr	Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser	Ser	210	215	220	



Pro	Pro	Ala	Val	Pro	Gln	Ser	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro	225	230	235	240
Thr	Gly	Ser	Gly	Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	245	250	255	
Gly	Tyr	Lys	Val	Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly	260	265	270	
Phe	Gly	Ala	Tyr	Met	Ser	Lys	Ala	His	Gly	Ile	Asp	Pro	Asn	Ile	Arg	275	280	285	
Thr	Gly	Val	Arg	Thr	Ile	Thr	Thr	Gly	Ala	Pro	Val	Thr	Tyr	Ser	Thr	290	295	300	
Tyr	Gly	Lys	Phe	Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	305	310	315	320
Ile	Ile	Ile	Cys	Asp	Glu	Cys	His	Ser	Thr	Asp	Ser	Thr	Thr	Ile	Leu	325	330	335	
Gly	Ile	Gly	Thr	Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	340	345	350	
Val	Val	Leu	Ala	Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Val	Pro	His	355	360	365	
Pro	Asn	Ile	Glu	Glu	Val	Ala	Leu	Ser	Asn	Thr	Gly	Glu	Ile	Pro	Phe	370	375	380	
Tyr	Gly	Lys	Ala	Ile	Pro	Ile	Glu	Ala	Ile	Arg	Gly	Gly	Arg	His	Leu	385	390	395	400
Ile	Phe	Cys	His	Ser	Lys	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Ala	Lys	Leu	405	410	415	
Ser	Gly	Leu	Gly	Ile	Asn	Ala	Val	Ala	Tyr	Tyr	Arg	Gly	Leu	Asp	Val	420	425	430	
Ser	Val	Ile	Pro	Thr	Ile	Gly	Asp	Val	Val	Val	Val	Ala	Thr	Asp	Ala	435	440	445	
Leu	Met	Thr	Gly	Tyr	Thr	Gly	Asp	Phe	Asp	Ser	Val	Ile	Asp	Cys	Asn	450	455	460	
Thr	Cys	Val	Thr	Gln	Thr	Val	Asp	Phe	Ser	Leu	Asp	Pro	Thr	Phe	Thr	465	470	475	480
Ile	Glu	Thr	Thr	Thr	Val	Pro	Gln	Asp	Ala	Val	Ser	Arg	Ser	Gln	Arg	485	490	495	
Arg	Gly	Arg	Thr	Gly	Arg	Gly	Arg	Arg	Gly	Ile	Tyr	Arg	Phe	Val	Thr	500	505	510	
Pro	Gly	Glu	Arg	Pro	Ser	Gly	Met	Phe	Asp	Ser	Ser	Val	Leu	Cys	Glu	515	520	525	
Cys	Tyr	Asp	Ala	Gly	Cys	Ala	Trp	Tyr	Glu	Leu	Thr	Pro	Ala	Glu	Thr				

530	535	540
Ser Val Arg Leu Arg	Ala Tyr Leu Asn Thr	Pro Gly Leu Pro Val Cys
545	550	555 560
Gln Asp His Leu Glu Phe Trp Glu Ser	Val Phe Thr Gly Leu Thr His	
	565 570	575
Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe		
	580 585	590
Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala		
	595 600	605
Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys		
	610 615	620
Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val		
	625 630	635 640
Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala		
	645 650	655
Cys Met Ser Ala Asp Leu Glu Val Val Thr		
	660 665	

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 666 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro	
1 5 10 15	
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	
20 25 30	
Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu	
35 40 45	
Leu Gly Cys Lys Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val	
50 55 60	
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala	
65 70 75 80	
Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser	
85 90 95	
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn	

100					105					110					
Val	Asp	Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser
	115						120					125			
Leu	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg
	130					135					140				
His	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser
145						150					155				160
Leu	Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly
				165					170					175	
Pro	Leu	Leu	Cys	Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala
			180					185					190		
Val	Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu
	195						200					205			
Ser	Met	Glu	Thr	Thr	Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser	Ser
	210					215					220				
Pro	Pro	Ala	Val	Pro	Gln	Ser	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro
225						230					235				240
Thr	Gly	Ser	Gly	Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln
				245					250					255	
Gly	Tyr	Lys	Val	Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly
			260					265					270		
Phe	Gly	Ala	Tyr	Met	Ser	Lys	Ala	His	Gly	Ile	Asp	Pro	Asn	Ile	Arg
	275						280					285			
Thr	Gly	Val	Arg	Thr	Ile	Thr	Thr	Gly	Ala	Pro	Val	Thr	Tyr	Ser	Thr
	290					295					300				
Tyr	Gly	Lys	Phe	Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp
305						310					315				320
Ile	Ile	Ile	Cys	Asp	Glu	Cys	His	Ser	Thr	Asp	Ser	Thr	Thr	Ile	Leu
				325					330					335	
Gly	Ile	Gly	Thr	Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu
			340					345					350		
Val	Val	Leu	Ala	Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Val	Pro	His
			355				360					365			
Pro	Asn	Ile	Glu	Glu	Val	Ala	Leu	Ser	Asn	Thr	Gly	Glu	Ile	Pro	Phe
	370					375					380				
Tyr	Gly	Lys	Ala	Ile	Pro	Ile	Glu	Ala	Ile	Arg	Gly	Gly	Arg	His	Leu
385						390					395				400
Ile	Phe	Cys	His	Ser	Lys	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Ala	Lys	Leu
				405					410					415	

Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val  
 420 425 430  
 Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala  
 435 440 445  
 Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn  
 450 455 460  
 Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr  
 465 470 475 480  
 Ile Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg  
 485 490 495  
 Arg Gly Arg Thr Gly Arg Gly Arg Arg Gly Ile Tyr Arg Phe Val Thr  
 500 505 510  
 Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu  
 515 520 525  
 Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr  
 530 535 540  
 Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys  
 545 550 555 560  
 Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His  
 565 570 575  
 Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe  
 580 585 590  
 Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala  
 595 600 605  
 Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys  
 610 615 620  
 Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val  
 625 630 635 640  
 Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala  
 645 650 655  
 Cys Met Ser Ala Asp Leu Glu Val Val Thr  
 660 665

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 666 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

75

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met	Gly	Ser	Ser	His	His	His	His	His	His	Ser	Ser	Gly	Leu	Val	Pro	1	5	10	15
Arg	Gly	Ser	His	Met	Gly	Ser	Val	Val	Ile	Val	Gly	Arg	Ile	Ile	Leu	20	25	30	
Ser	Gly	Ser	Gly	Ser	Ile	Thr	Ala	Tyr	Ser	Gln	Gln	Thr	Arg	Gly	Leu	35	40	45	
Leu	Gly	Cys	Ile	Ile	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val	50	55	60	
Glu	Gly	Glu	Val	Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala	65	70	75	80
Thr	Cys	Val	Asn	Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser	85	90	95	
Lys	Thr	Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	100	105	110	
Val	Asp	Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	115	120	125	
Leu	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	130	135	140	
His	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	145	150	155	160
Leu	Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ala	Gly	Gly	165	170	175	
Pro	Leu	Leu	Cys	Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	180	185	190	
Val	Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	195	200	205	
Ser	Met	Glu	Thr	Thr	Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser	Ser	210	215	220	
Pro	Pro	Ala	Val	Pro	Gln	Ser	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro	225	230	235	240
Thr	Gly	Ser	Gly	Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	245	250	255	
Gly	Tyr	Lys	Val	Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly	260	265	270	
Phe	Gly	Ala	Tyr	Met	Ser	Lys	Ala	His	Gly	Ile	Asp	Pro	Asn	Ile	Arg	275	280	285	

Thr	Gly	Val	Arg	Thr	Ile	Thr	Thr	Gly	Ala	Pro	Val	Thr	Tyr	Ser	Thr	290	295	300	
Tyr	Gly	Lys	Phe	Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	305	310	315	320
Ile	Ile	Ile	Cys	Asp	Glu	Cys	His	Ser	Thr	Asp	Ser	Thr	Thr	Ile	Leu	325	330	335	
Gly	Ile	Gly	Thr	Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	340	345	350	
Val	Val	Leu	Ala	Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Val	Pro	His	355	360	365	
Pro	Asn	Ile	Glu	Glu	Val	Ala	Leu	Ser	Asn	Thr	Gly	Glu	Ile	Pro	Phe	370	375	380	
Tyr	Gly	Lys	Ala	Ile	Pro	Ile	Glu	Ala	Ile	Arg	Gly	Gly	Arg	His	Leu	385	390	395	400
Ile	Phe	Cys	His	Ser	Lys	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Ala	Lys	Leu	405	410	415	
Ser	Gly	Leu	Gly	Ile	Asn	Ala	Val	Ala	Tyr	Tyr	Arg	Gly	Leu	Asp	Val	420	425	430	
Ser	Val	Ile	Pro	Thr	Ile	Gly	Asp	Val	Val	Val	Val	Ala	Thr	Asp	Ala	435	440	445	
Leu	Met	Thr	Gly	Tyr	Thr	Gly	Asp	Phe	Asp	Ser	Val	Ile	Asp	Cys	Asn	450	455	460	
Thr	Cys	Val	Thr	Gln	Thr	Val	Asp	Phe	Ser	Leu	Asp	Pro	Thr	Phe	Thr	465	470	475	480
Ile	Glu	Thr	Thr	Thr	Val	Pro	Gln	Asp	Ala	Val	Ser	Arg	Ser	Gln	Arg	485	490	495	
Arg	Gly	Arg	Thr	Gly	Arg	Gly	Arg	Arg	Gly	Ile	Tyr	Arg	Phe	Val	Thr	500	505	510	
Pro	Gly	Glu	Arg	Pro	Ser	Gly	Met	Phe	Asp	Ser	Ser	Val	Leu	Cys	Glu	515	520	525	
Cys	Tyr	Asp	Ala	Gly	Cys	Ala	Trp	Tyr	Glu	Leu	Thr	Pro	Ala	Glu	Thr	530	535	540	
Ser	Val	Arg	Leu	Arg	Ala	Tyr	Leu	Asn	Thr	Pro	Gly	Leu	Pro	Val	Cys	545	550	555	560
Gln	Asp	His	Leu	Glu	Phe	Trp	Glu	Ser	Val	Phe	Thr	Gly	Leu	Thr	His	565	570	575	
Ile	Asp	Ala	His	Phe	Leu	Ser	Gln	Thr	Lys	Gln	Ala	Gly	Asp	Asn	Phe	580	585	590	
Pro	Tyr	Leu	Val	Ala	Tyr	Gln	Ala	Thr	Val	Cys	Ala	Arg	Ala	Gln	Ala				

595	600	605
Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys		
610	615	620
Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val		
625	630	635 640
Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala		
	645	650 655
Cys Met Ser Ala Asp Leu Glu Val Val Thr		
	660	665

## (2) INFORMATION FOR SEQ ID NO:16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro		
1	5	10 15
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu		
	20	25 30
Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu		
	35	40 45
Leu Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val		
	50	55 60
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala		
	65	70 75 80
Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser		
	85	90 95
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn		
	100	105 110
Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser		
	115	120 125
Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg		
	130	135 140
His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser		
	145	150 155 160
Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly		

				165				170				175			
Pro	Leu	Leu	Cys 180	Pro	Ser	Gly	His	Ala 185	Val	Gly	Ile	Phe	Arg 190	Ala	Ala
Val	Cys	Thr 195	Arg	Gly	Val	Ala	Lys 200	Ala	Val	Asp	Phe	Val 205	Pro	Val	Glu
Ser	Met 210	Glu	Thr	Thr	Met	Arg 215	Ser	Pro	Val	Phe	Thr 220	Asp	Asn	Ser	Ser
Pro 225	Pro	Ala	Val	Pro	Gln 230	Ser	Phe	Gln	Val	Ala 235	His	Leu	His	Ala	Pro 240
Thr	Gly	Ser	Gly	Lys 245	Ser	Thr	Lys	Val	Pro 250	Ala	Ala	Tyr	Ala	Ala	Gln 255
Gly	Tyr	Lys	Val 260	Leu	Val	Leu	Asn	Pro 265	Ser	Val	Ala	Ala	Thr 270	Leu	Gly
Phe	Gly	Ala 275	Tyr	Met	Ser	Lys	Ala 280	His	Gly	Ile	Asp	Pro 285	Asn	Ile	Arg
Thr	Gly 290	Val	Arg	Thr	Ile	Thr 295	Thr	Gly	Ala	Pro	Val 300	Thr	Tyr	Ser	Thr
Tyr 305	Gly	Lys	Phe	Leu	Ala 310	Asp	Gly	Gly	Cys	Ser 315	Gly	Gly	Ala	Tyr	Asp 320
Ile	Ile	Ile	Cys	Asp 325	Glu	Cys	His	Ser	Thr 330	Asp	Ser	Thr	Thr	Ile	Leu 335
Gly	Ile	Gly	Thr 340	Val	Leu	Asp	Gln	Ala 345	Glu	Thr	Ala	Gly	Ala 350	Arg	Leu
Val	Val	Leu 355	Ala	Thr	Ala	Thr	Pro 360	Pro	Gly	Ser	Val	Thr 365	Val	Pro	His
Pro 370	Asn	Ile	Glu	Glu	Val	Ala 375	Leu	Ser	Asn	Thr	Gly 380	Glu	Ile	Pro	Phe
Tyr 385	Gly	Lys	Ala	Ile	Pro 390	Ile	Glu	Ala	Ile	Arg 395	Gly	Gly	Arg	His	Leu 400
Ile	Phe	Cys	His 405	Ser	Lys	Lys	Lys	Cys	Asp 410	Glu	Leu	Ala	Ala	Lys	Leu 415
Ser	Gly	Leu	Gly 420	Ile	Asn	Ala	Val	Ala 425	Tyr	Tyr	Arg	Gly	Leu 430	Asp	Val
Ser	Val	Ile 435	Pro	Thr	Ile	Gly	Asp 440	Val	Val	Val	Val	Ala 445	Thr	Asp	Ala
Leu	Met 450	Thr	Gly	Tyr	Thr	Gly 455	Asp	Phe	Asp	Ser	Val 460	Ile	Asp	Cys	Asn
Thr 465	Cys	Val	Thr	Gln	Thr 470	Val	Asp	Phe	Ser	Leu 475	Asp	Pro	Thr	Phe	Thr 480



Ile Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg  
 485 490 495  
 Arg Gly Arg Thr Gly Arg Gly Arg Arg Gly Ile Tyr Arg Phe Val Thr  
 500 505 510  
 Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu  
 515 520 525  
 Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr  
 530 535 540  
 Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys  
 545 550 555 560  
 Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His  
 565 570 575  
 Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe  
 580 585 590  
 Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala  
 595 600 605  
 Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys  
 610 615 620  
 Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val  
 625 630 635 640  
 Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala  
 645 650 655  
 Cys Met Ser Ala Asp Leu Glu Val Val Thr  
 660 665

## (2) INFORMATION FOR SEQ ID NO:17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro  
 1 5 10 15  
 Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu  
 20 25 30  
 Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu  
 35 40 45

Leu	Gly	Cys	Ile	Lys	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val	50	55	60
Glu	Gly	Glu	Val	Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala	65	70	75
Thr	Cys	Val	Asn	Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser	85	90	95
Lys	Thr	Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	100	105	110
Val	Asp	Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	115	120	125
Leu	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	130	135	140
His	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	145	150	155
Leu	Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ala	Gly	Gly	165	170	175
Pro	Leu	Leu	Cys	Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	180	185	190
Val	Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	195	200	205
Ser	Met	Glu	Thr	Thr	Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser	Ser	210	215	220
Pro	Pro	Ala	Val	Pro	Gln	Ser	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro	225	230	235
Thr	Gly	Ser	Gly	Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	245	250	255
Gly	Tyr	Lys	Val	Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly	260	265	270
Phe	Gly	Ala	Tyr	Met	Ser	Lys	Ala	His	Gly	Ile	Asp	Pro	Asn	Ile	Arg	275	280	285
Thr	Gly	Val	Arg	Thr	Ile	Thr	Thr	Gly	Ala	Pro	Val	Thr	Tyr	Ser	Thr	290	295	300
Tyr	Gly	Lys	Phe	Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	305	310	315
Ile	Ile	Ile	Cys	Asp	Glu	Cys	His	Ser	Thr	Asp	Ser	Thr	Thr	Ile	Leu	325	330	335
Gly	Ile	Gly	Thr	Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	340	345	350

Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His  
 355 360 365  
 Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe  
 370 375 380  
 Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu  
 385 390 395 400  
 Ile Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu  
 405 410 415  
 Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val  
 420 425 430  
 Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala  
 435 440 445  
 Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn  
 450 455 460  
 Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr  
 465 470 475 480  
 Ile Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg  
 485 490 495  
 Arg Gly Arg Thr Gly Arg Gly Arg Arg Gly Ile Tyr Arg Phe Val Thr  
 500 505 510  
 Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu  
 515 520 525  
 Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr  
 530 535 540  
 Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys  
 545 550 555 560  
 Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His  
 565 570 575  
 Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe  
 580 585 590  
 Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala  
 595 600 605  
 Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys  
 610 615 620  
 Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val  
 625 630 635 640  
 Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala  
 645 650 655  
 Cys Met Ser Ala Asp Leu Glu Val Val Thr

660

665

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 666 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
 1           5           10           15

Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu
 20           25           30

Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu
 35           40           45

Leu Gly Cys Lys Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val
 50           55           60

Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala
 65           70           75           80

Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser
 85           90           95

Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn
100          105          110

Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser
115          120          125

Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg
130          135          140

His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser
145          150          155          160

Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly
165          170          175

Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala
180          185          190

Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu
195          200          205

Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser
210          215          220

Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro

```

225		230		235		240
Thr Gly Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln						
		245		250		255
Gly Tyr Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly						
		260		265		270
Phe Gly Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg						
		275		280		285
Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr						
		290		295		300
Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp						
305		310		315		320
Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu						
		325		330		335
Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu						
		340		345		350
Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His						
		355		360		365
Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe						
		370		375		380
Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu						
385		390		395		400
Ile Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu						
		405		410		415
Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val						
		420		425		430
Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala						
		435		440		445
Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn						
		450		455		460
Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr						
465		470		475		480
Ile Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg						
		485		490		495
Arg Gly Arg Thr Gly Arg Gly Arg Arg Gly Ile Tyr Arg Phe Val Thr						
		500		505		510
Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu						
		515		520		525
Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr						
		530		535		540

Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys  
 545 550 555 560  
 Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His  
 565 570 575  
 Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe  
 580 585 590  
 Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala  
 595 600 605  
 Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys  
 610 615 620  
 Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val  
 625 630 635 640  
 Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala  
 645 650 655  
 Cys Met Ser Ala Asp Leu Glu Val Val Thr  
 660 665

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 672 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro  
 1 5 10 15  
 Arg Gly Ser His Met Ala Tyr Ser Leu Thr Thr Gly Ser Val Val Ile  
 20 25 30  
 Val Gly Arg Ile Ile Leu Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser  
 35 40 45  
 Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly  
 50 55 60  
 Arg Asp Lys Asn Gln Val Glu Gly Glu Val Gln Val Val Ser Thr Ala  
 65 70 75 80  
 Thr Gln Ser Phe Leu Ala Thr Cys Val Asn Gly Val Cys Trp Thr Val  
 85 90 95  
 Tyr His Gly Ala Gly Ser Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile  
 100 105 110

85

Thr	Gln	Met	Tyr	Thr	Asn	Val	Asp	Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala	
		115					120					125				
Pro	Pro	Gly	Ala	Arg	Ser	Leu	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	
		130				135					140					
Leu	Tyr	Leu	Val	Thr	Arg	His	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	
145					150					155					160	
Gly	Asp	Ser	Arg	Gly	Ser	Leu	Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	
				165					170					175		
Lys	Gly	Ser	Ser	Gly	Gly	Pro	Leu	Leu	Cys	Pro	Ser	Gly	His	Ala	Val	
			180					185					190			
Gly	Ile	Phe	Arg	Ala	Ala	Val	Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	
		195					200					205				
Asp	Phe	Val	Pro	Val	Glu	Ser	Met	Glu	Thr	Thr	Met	Arg	Ser	Pro	Val	
		210				215					220					
Phe	Thr	Asp	Asn	Ser	Ser	Pro	Pro	Ala	Val	Pro	Gln	Ser	Phe	Gln	Val	
225					230					235					240	
Ala	His	Leu	His	Ala	Pro	Thr	Gly	Ser	Gly	Lys	Ser	Thr	Lys	Val	Pro	
				245					250					255		
Ala	Ala	Tyr	Ala	Ala	Gln	Gly	Tyr	Lys	Val	Leu	Val	Leu	Asn	Pro	Ser	
			260					265					270			
Val	Ala	Ala	Thr	Leu	Gly	Phe	Gly	Ala	Tyr	Met	Ser	Lys	Ala	His	Gly	
			275				280					285				
Ile	Asp	Pro	Asn	Ile	Arg	Thr	Gly	Val	Arg	Thr	Ile	Thr	Thr	Gly	Ala	
	290					295					300					
Pro	Val	Thr	Tyr	Ser	Thr	Tyr	Gly	Lys	Phe	Leu	Ala	Asp	Gly	Gly	Cys	
305					310					315					320	
Ser	Gly	Gly	Ala	Tyr	Asp	Ile	Ile	Ile	Cys	Asp	Glu	Cys	His	Ser	Thr	
				325					330					335		
Asp	Ser	Thr	Thr	Ile	Leu	Gly	Ile	Gly	Thr	Val	Leu	Asp	Gln	Ala	Glu	
			340					345					350			
Thr	Ala	Gly	Ala	Arg	Leu	Val	Val	Leu	Ala	Thr	Ala	Thr	Pro	Pro	Gly	
		355					360					365				
Ser	Val	Thr	Val	Pro	His	Pro	Asn	Ile	Glu	Glu	Val	Ala	Leu	Ser	Asn	
						375					380					
Thr	Gly	Glu	Ile	Pro	Phe	Tyr	Gly	Lys	Ala	Ile	Pro	Ile	Glu	Ala	Ile	
385					390					395					400	
Arg	Gly	Gly	Arg	His	Leu	Ile	Phe	Cys	His	Ser	Lys	Lys	Lys	Cys	Asp	
				405					410					415		

Glu Leu Ala Ala Lys Leu Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr  
                   420                                  425                                  430  
 Tyr Arg Gly Leu Asp Val Ser Val Ile Pro Thr Ile Gly Asp Val Val  
                   435                                  440                                  445  
 Val Val Ala Thr Asp Ala Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp  
                   450                                  455                                  460  
 Ser Val Ile Asp Cys Asn Thr Cys Val Thr Gln Thr Val Asp Phe Ser  
 465                                  470                                  475                                  480  
 Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr Thr Val Pro Gln Asp Ala  
                                   485                                  490                                  495  
 Val Ser Arg Ser Gln Arg Arg Gly Arg Thr Gly Arg Gly Arg Arg Gly  
                                   500                                  505                                  510  
 Ile Tyr Arg Phe Val Thr Pro Gly Glu Arg Pro Ser Gly Met Phe Asp  
                   515                                  520                                  525  
 Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu  
                   530                                  535                                  540  
 Leu Thr Pro Ala Glu Thr Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr  
 545                                  550                                  555                                  560  
 Pro Gly Leu Pro Val Cys Gln Asp His Leu Glu Phe Trp Glu Ser Val  
                                   565                                  570                                  575  
 Phe Thr Gly Leu Thr His Ile Asp Ala His Phe Leu Ser Gln Thr Lys  
                   580                                  585                                  590  
 Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val  
                   595                                  600                                  605  
 Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser Trp Asp Gln Met Trp Lys  
                   610                                  615                                  620  
 Cys Leu Ile Arg Leu Lys Pro Thr Leu His Gly Pro Thr Pro Leu Leu  
 625                                  630                                  635                                  640  
 Tyr Arg Leu Gly Ala Val Gln Asn Glu Val Thr Leu Thr His Pro Ile  
                   645                                  650                                  655  
 Thr Lys Tyr Ile Met Ala Cys Met Ser Ala Asp Leu Glu Val Val Thr  
                   660                                  665                                  670

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 672 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met	Gly	Ser	Ser	His	His	His	His	His	His	Ser	Ser	Gly	Leu	Val	Pro	1	5	10	15
Arg	Gly	Ser	His	Met	Ala	Tyr	Ser	Leu	Thr	Thr	Gly	Ser	Val	Val	Ile	20	25	30	
Val	Gly	Arg	Ile	Ile	Leu	Ser	Gly	Ser	Gly	Ser	Ile	Thr	Ala	Tyr	Ser	35	40	45	
Gln	Gln	Thr	Arg	Gly	Leu	Leu	Gly	Cys	Ile	Ile	Thr	Ser	Leu	Thr	Gly	50	55	60	
Arg	Asp	Lys	Asn	Gln	Val	Glu	Gly	Glu	Val	Gln	Val	Val	Ser	Thr	Ala	65	70	75	80
Thr	Gln	Ser	Phe	Leu	Ala	Thr	Cys	Val	Asn	Gly	Val	Cys	Trp	Thr	Val	85	90	95	
Tyr	His	Gly	Ala	Gly	Ser	Lys	Thr	Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile	100	105	110	
Thr	Gln	Met	Tyr	Thr	Asn	Val	Asp	Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala	115	120	125	
Pro	Pro	Gly	Ala	Arg	Ser	Leu	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	130	135	140	
Leu	Tyr	Leu	Val	Thr	Arg	His	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	145	150	155	160
Gly	Asp	Ser	Arg	Gly	Ser	Leu	Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	165	170	175	
Lys	Gly	Ser	Ala	Gly	Gly	Pro	Leu	Leu	Cys	Pro	Ser	Gly	His	Ala	Val	180	185	190	
Gly	Ile	Phe	Arg	Ala	Ala	Val	Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	195	200	205	
Asp	Phe	Val	Pro	Val	Glu	Ser	Met	Glu	Thr	Thr	Met	Arg	Ser	Pro	Val	210	215	220	
Phe	Thr	Asp	Asn	Ser	Ser	Pro	Pro	Ala	Val	Pro	Gln	Ser	Phe	Gln	Val	225	230	235	240
Ala	His	Leu	His	Ala	Pro	Thr	Gly	Ser	Gly	Lys	Ser	Thr	Lys	Val	Pro	245	250	255	
Ala	Ala	Tyr	Ala	Ala	Gln	Gly	Tyr	Lys	Val	Leu	Val	Leu	Asn	Pro	Ser	260	265	270	
Val	Ala	Ala	Thr	Leu	Gly	Phe	Gly	Ala	Tyr	Met	Ser	Lys	Ala	His	Gly	275	280	285	
Ile	Asp	Pro	Asn	Ile	Arg	Thr	Gly	Val	Arg	Thr	Ile	Thr	Thr	Gly	Ala				

290		295		300
Pro Val Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys				
305		310		315 320
Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys Asp Glu Cys His Ser Thr				
	325		330	335
Asp Ser Thr Thr Ile Leu Gly Ile Gly Thr Val Leu Asp Gln Ala Glu				
	340		345	350
Thr Ala Gly Ala Arg Leu Val Val Leu Ala Thr Ala Thr Pro Pro Gly				
	355		360	365
Ser Val Thr Val Pro His Pro Asn Ile Glu Glu Val Ala Leu Ser Asn				
	370		375	380
Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile				
385		390		395 400
Arg Gly Gly Arg His Leu Ile Phe Cys His Ser Lys Lys Lys Cys Asp				
	405		410	415
Glu Leu Ala Ala Lys Leu Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr				
	420		425	430
Tyr Arg Gly Leu Asp Val Ser Val Ile Pro Thr Ile Gly Asp Val Val				
	435		440	445
Val Val Ala Thr Asp Ala Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp				
	450		455	460
Ser Val Ile Asp Cys Asn Thr Cys Val Thr Gln Thr Val Asp Phe Ser				
465		470		475 480
Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr Thr Val Pro Gln Asp Ala				
	485		490	495
Val Ser Arg Ser Gln Arg Arg Gly Arg Thr Gly Arg Gly Arg Arg Gly				
	500		505	510
Ile Tyr Arg Phe Val Thr Pro Gly Glu Arg Pro Ser Gly Met Phe Asp				
	515		520	525
Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu				
	530		535	540
Leu Thr Pro Ala Glu Thr Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr				
545		550		555 560
Pro Gly Leu Pro Val Cys Gln Asp His Leu Glu Phe Trp Glu Ser Val				
	565		570	575
Phe Thr Gly Leu Thr His Ile Asp Ala His Phe Leu Ser Gln Thr Lys				
	580		585	590
Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val				
	595		600	605

Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser Trp Asp Gln Met Trp Lys  
 610 615 620

Cys Leu Ile Arg Leu Lys Pro Thr Leu His Gly Pro Thr Pro Leu Leu  
 625 630 635 640

Tyr Arg Leu Gly Ala Val Gln Asn Glu Val Thr Leu Thr His Pro Ile  
 645 650 655

Thr Lys Tyr Ile Met Ala Cys Met Ser Ala Asp Leu Glu Val Val Thr  
 660 665 670

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Gly Ser Gly Ser  
 1

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Pro Ala Gly Gly  
 1

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 632 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein .

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met	Ala	Pro	Ile	Thr	Ala	Tyr	Ser	Gln	Gln	Thr	Arg	Gly	Leu	Leu	Gly	1	5	10	15
Cys	Ile	Ile	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val	Glu	Gly	20	25	30	
Glu	Val	Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala	Thr	Cys	35	40	45	
Val	Asn	Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser	Lys	Thr	50	55	60	
Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	Val	Asp	65	70	75	
Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	Leu	Thr	85	90	95	
Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	His	Ala	100	105	110	
Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	Leu	Leu	115	120	125	
Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly	Pro	Leu	130	135	140	
Leu	Cys	Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	Val	Cys	145	150	155	
Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	Ser	Met	165	170	175	
Glu	Thr	Thr	Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser	Ser	Pro	Pro	180	185	190	
Ala	Val	Pro	Gln	Ser	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro	Thr	Gly	195	200	205	
Ser	Gly	Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	Gly	Tyr	210	215	220	
Lys	Val	Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly	Phe	Gly	225	230	235	
Ala	Tyr	Met	Ser	Lys	Ala	His	Gly	Ile	Asp	Pro	Asn	Ile	Arg	Thr	Gly	245	250	255	
Val	Arg	Thr	Ile	Thr	Thr	Gly	Ala	Pro	Val	Thr	Tyr	Ser	Thr	Tyr	Gly	260	265	270	
Lys	Phe	Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	Ile	Ile				

275	280	285
Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu Gly Ile		
290	295	300
Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val		
305	310	315
Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn		
	325	330
Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe Tyr Gly		
	340	345
Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu Ile Phe		
	355	360
Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Ser Gly		
	370	375
Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val		
385	390	395
Ile Pro Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala Leu Met		
	405	410
Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys		
	420	425
Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu		
	435	440
Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly		
	450	455
Arg Thr Gly Arg Gly Arg Arg Gly Ile Tyr Arg Phe Val Thr Pro Gly		
465	470	475
Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr		
	485	490
Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Ser Val		
	500	505
Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp		
	515	520
His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp		
	530	535
Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr		
545	550	555
Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro		
	565	570
Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr		
	580	585
		590

Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn  
 595 600 605  
 Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met  
 610 615 620  
 Ser Ala Asp Leu Glu Val Val Thr  
 625 630

## (2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 54 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Ser Thr Trp Val Leu Val Gly Gly Val Leu Ala Ala Leu Ala Ala Tyr  
 1 5 10 15  
 Cys Leu Thr Thr Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu Ser  
 20 25 30  
 Gly Arg Pro Ala Ile Val Pro Asp Arg Glu Leu Leu Tyr Gln Glu Phe  
 35 40 45  
 Asp Glu Met Glu Glu Cys  
 50

## (2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Asp Thr Glu Asp Val Val Cys Cys Ser Met Tyr Thr Trp Thr Gly Lys  
 1 5 10 15

## (2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 78 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GATATACATA TGGGTTCTGT TGTTATTGTT GGTAGAATTA TTTTATCTGG TAGTGGTAGT 60  
ATCACGGCCT ACTCCCAA 78

## (2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTCAGCGAAT TCTCAAGACC GCATAGTAGT TTCCAT 36

## (2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CGGGGCCTAC TTGGTTGCAA GATCACTAGC CTTACAGGC 39

## (2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GCCTGTAAGG CTAGTGATCT TGCAACCAAG TAGGCCCCCG

39

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CGGGGCCTAC TTGGTTGCAT CAAGACTAGC CTTACAGGC

39

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GCCTGTAAGG CTAGTCTTGA TGCAACCAAG TAGGCCCCCG

39

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

95



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CGGGGCCTAC TTGGTTGCAA GAAGACTAGC CTTACAGGC

39

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GCCTGTAAGG CTAGTCTTCT TGCAACCAAG TAGGCCCCG

39

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CTCCTACTTG AAGGGCTCTG CTGGTGGTCC ACTGCTCTGC

40

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GCAGAGCAGT GGACCACCAG CAGAGCCCTT CAAGTAGGAG

40

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:

96

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CGGGGCCTAC TTGGTTGCAA GATCACTAGC CTTACAGGC

39

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCCTGTAAGG CTAGTGATCT TGCAACCAAG TAGGCCCCG

39

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CGGGGCCTAC TTGGTTGCAT CAAGACTAGC CTTACAGGC

39

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GCCTGTAAGG CTAGTCTTGA TGCAACCAAG TAGGCCCCG

39

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CGGGGCCTAC TTGGTTGCAA GAAGACTAGC CTTACAGGC

39

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GCCTGTAAGG CTAGTCTTGA TGCAACCAAG TAGGCCCCG

39

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GATATACATA TGGGTTCTGT TGTTATTGTT GGTAGAATTA TTTTATCTCC TGCTGGTGTT

60

ATCACGGCCT ACTCCCAA

78

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 36 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTCAGCGAAT TCTCAAGACC GCATAGTAGT TTCCAT

36

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 39 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CGGGGCCTAC TTGGTTGCAA GATCACTAGC CTTACAGGC

39

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 39 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GCCTGTAAGG CTAGTGATCT TGCAACCAAG TAGGCCCCG

39

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 215 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met	Gly	Ser	Ser	His	His	His	His	His	His	Ser	Ser	Gly	Leu	Val	Pro	1	5	10	15
Arg	Gly	Ser	His	Met	Gly	Ser	Val	Val	Ile	Val	Gly	Arg	Ile	Ile	Leu	20	25	30	
Ser	Pro	Ala	Gly	Ile	Thr	Ala	Tyr	Ser	Gln	Gln	Thr	Arg	Gly	Leu	Leu	35	40	45	
Gly	Cys	Ile	Ile	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val	Glu	50	55	60	
Gly	Glu	Val	Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala	Thr	65	70	75	80
Cys	Val	Asn	Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser	Lys	85	90	95	
Thr	Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	Val	100	105	110	
Asp	Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	Leu	115	120	125	
Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	His	130	135	140	
Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	Leu	145	150	155	160
Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly	Pro	165	170	175	
Leu	Leu	Cys	Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	Val	180	185	190	
Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	Ser	195	200	205	
Met	Glu	Thr	Thr	Met	Arg	Ser										210	215		

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Pro Ala Gly  
1

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 75 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GATATACATA TGGGTTCTGT TGTTATTGTT GGTAGAATTA TTTTATCTCC TGCTGGTATC	60
ACGGCCTACT CCAA	75

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 36 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CTCAGCGAAT TCTCAAGACC GCATAGTAGT TTCCAT	36
---	----

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 215 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro  
 1 5 10 15  
 Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu  
 20 25 30  
 Ser Pro Ala Gly Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu  
 35 40 45  
 Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu  
 50 55 60  
 Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr  
 65 70 75 80  
 Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys  
 85 90 95  
 Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val  
 100 105 110  
 Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu  
 115 120 125  
 Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His  
 130 135 140  
 Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu  
 145 150 155 160  
 Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro  
 165 170 175  
 Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val  
 180 185 190  
 Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser  
 195 200 205  
 Met Glu Thr Thr Met Arg Ser  
 210 215

## (2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CGGGGCCTAC TTGGTTGCAA GATCACTAGC CTTACAGGC

39

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GCCTGTAAGG CTAGTGATCT TGCAACCAAG TAGGCCCCG

39

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 215 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Met	Gly	Ser	Ser	His	His	His	His	His	His	Ser	Ser	Gly	Leu	Val	Pro	1	5	10	15
Arg	Gly	Ser	His	Met	Gly	Ser	Val	Val	Ile	Val	Gly	Arg	Ile	Ile	Leu	20	25	30	
Ser	Gly	Gly	Ser	Ile	Thr	Ala	Tyr	Ser	Gln	Gln	Thr	Arg	Gly	Leu	Leu	35	40	45	
Gly	Cys	Ile	Ile	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val	Glu	50	55	60	
Gly	Glu	Val	Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala	Thr	65	70	75	80
Cys	Val	Asn	Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser	Lys	85	90	95	
Thr	Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	Val	100	105	110	
Asp	Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	Leu	115	120	125	
Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	His	130	135	140	



Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	Leu
145					150					155					160
Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly	Pro
				165					170					175	
Leu	Leu	Cys	Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	Val
			180					185					190		
Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	Ser
		195					200					205			
Met	Glu	Thr	Thr	Met	Arg	Ser									
	210					215									

## (2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Gly Gly Ser  
1

## (2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 75 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GATATACATA TGGGTTCTGT TGTTATTGTT GGTAGAATTA TTTTATCTGG TGTTCTATC	60
ACGGCCTACT CCCAA	75

## (2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

36

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 215 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

165

Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val  
                   180                                  185                                  190

Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser  
                   195                                  200                                  205

Met Glu Thr Thr Met Arg Ser  
           210                                  215

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CGGGGCCTAC TTGGTTGCAA GATCACTAGC CTTACAGGC

39

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GCCTGTAAGG CTAGTGATCT TGCAACCAAG TAGGCCCCG

39

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 646 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Met His Met His His His His His His Leu Val Pro Arg Gly Ser Ala  
       1                                  5                                  10                                  15

Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly Cys Lys

20					25					30					
Ile	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val	Glu	Gly	Glu	Val
		35					40					45			
Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala	Thr	Cys	Val	Asn
	50					55					60				
Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser	Lys	Thr	Leu	Ala
65					70					75					80
Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	Val	Asp	Gln	Asp
				85					90					95	
Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	Leu	Thr	Pro	Cys
			100					105					110		
Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	His	Ala	Asp	Val
		115					120					125			
Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	Leu	Leu	Ser	Pro
	130					135					140				
Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly	Pro	Leu	Leu	Cys
145					150					155					160
Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	Val	Cys	Thr	Arg
				165					170					175	
Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	Ser	Met	Glu	Thr
			180					185					190		
Thr	Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser	Ser	Pro	Pro	Ala	Val
		195					200					205			
Pro	Gln	Ser	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro	Thr	Gly	Ser	Gly
	210					215					220				
Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	Gly	Tyr	Lys	Val
225					230					235					240
Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly	Phe	Gly	Ala	Tyr
				245					250					255	
Met	Ser	Lys	Ala	His	Gly	Ile	Asp	Pro	Asn	Ile	Arg	Thr	Gly	Val	Arg
			260					265					270		
Thr	Ile	Thr	Thr	Gly	Ala	Pro	Val	Thr	Tyr	Ser	Thr	Tyr	Gly	Lys	Phe
		275					280					285			
Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	Ile	Ile	Ile	Cys
	290					295					300				
Asp	Glu	Cys	His	Ser	Thr	Asp	Ser	Thr	Thr	Ile	Leu	Gly	Ile	Gly	Thr
305					310					315					320
Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	Val	Val	Leu	Ala
				325					330					335	

Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Val	Pro	His	Pro	Asn	Ile	Glu		
			340					345					350				
Glu	Val	Ala	Leu	Ser	Asn	Thr	Gly	Glu	Ile	Pro	Phe	Tyr	Gly	Lys	Ala		
		355					360					365					
Ile	Pro	Ile	Glu	Ala	Ile	Arg	Gly	Gly	Arg	His	Leu	Ile	Phe	Cys	His		
	370					375					380						
Ser	Lys	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Ala	Lys	Leu	Ser	Gly	Leu	Gly		
385					390					395					400		
Ile	Asn	Ala	Val	Ala	Tyr	Tyr	Arg	Gly	Leu	Asp	Val	Ser	Val	Ile	Pro		
				405					410					415			
Thr	Ile	Gly	Asp	Val	Val	Val	Val	Ala	Thr	Asp	Ala	Leu	Met	Thr	Gly		
			420					425					430				
Tyr	Thr	Gly	Asp	Phe	Asp	Ser	Val	Ile	Asp	Cys	Asn	Thr	Cys	Val	Thr		
		435					440					445					
Gln	Thr	Val	Asp	Phe	Ser	Leu	Asp	Pro	Thr	Phe	Thr	Ile	Glu	Thr	Thr		
	450					455					460						
Thr	Val	Pro	Gln	Asp	Ala	Val	Ser	Arg	Ser	Gln	Arg	Arg	Gly	Arg	Thr		
465					470					475					480		
Gly	Arg	Gly	Arg	Arg	Gly	Ile	Tyr	Arg	Phe	Val	Thr	Pro	Gly	Glu	Arg		
				485					490					495			
Pro	Ser	Gly	Met	Phe	Asp	Ser	Ser	Val	Leu	Cys	Glu	Cys	Tyr	Asp	Ala		
			500					505					510				
Gly	Cys	Ala	Trp	Tyr	Glu	Leu	Thr	Pro	Ala	Glu	Thr	Ser	Val	Arg	Leu		
		515					520					525					
Arg	Ala	Tyr	Leu	Asn	Thr	Pro	Gly	Leu	Pro	Val	Cys	Gln	Asp	His	Leu		
	530					535					540						
Glu	Phe	Trp	Glu	Ser	Val	Phe	Thr	Gly	Leu	Thr	His	Ile	Asp	Ala	His		
545					550					555					560		
Phe	Leu	Ser	Gln	Thr	Lys	Gln	Ala	Gly	Asp	Asn	Phe	Pro	Tyr	Leu	Val		
				565					570					575			
Ala	Tyr	Gln	Ala	Thr	Val	Cys	Ala	Arg	Ala	Gln	Ala	Pro	Pro	Pro	Ser		
			580					585					590				
Trp	Asp	Gln	Met	Trp	Lys	Cys	Leu	Ile	Arg	Leu	Lys	Pro	Thr	Leu	His		
		595					600						605				
Gly	Pro	Thr	Pro	Leu	Leu	Tyr	Arg	Leu	Gly	Ala	Val	Gln	Asn	Glu	Val		
	610					615					620						
Thr	Leu	Thr	His	Pro	Ile	Thr	Lys	Tyr	Ile	Met	Ala	Cys	Met	Ser	Ala		
625					630					635					640		

Asp Leu Glu Val Val Thr  
645

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CGGGGCCTAC TTGGTTGCAA GATCACTAGC CTTACAGGC

39

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GCCTGTAAGG CTAGTGATCT TGCAACCAAG TAGGCCCCG

39

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 646 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met His Met His His His His His His Leu Val Pro Arg Gly Ser Ala  
1 5 10 15

Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile  
20 25 30

Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly Glu Val

35		40		45
Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys Val Asn	50	55	60	
Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr Leu Ala	65	70	75	80
Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp Gln Asp		85	90	95
Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys		100	105	110
Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala Asp Val	115		120	125
Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro	130	135		140
Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu Leu Cys	145	150	155	160
Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys Thr Arg		165	170	175
Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser Met Glu Thr		180	185	190
Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro Ala Val	195		200	205
Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro Thr Gly Ser Gly	210	215		220
Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val	225	230	235	240
Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr		245	250	255
Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly Val Arg		260	265	270
Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly Lys Phe	275		280	285
Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys	290	295		300
Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu Gly Ile Gly Thr	305	310	315	320
Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala		325	330	335
Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn Ile Glu		340	345	350

Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala  
 355 360 365  
 Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu Ile Phe Cys His  
 370 375 380  
 Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Ser Gly Leu Gly  
 385 390 395 400  
 Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val Ile Pro  
 405 410 415  
 Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala Leu Met Thr Gly  
 420 425 430  
 Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys Val Thr  
 435 440 445  
 Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr  
 450 455 460  
 Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly Arg Thr  
 465 470 475 480  
 Gly Arg Gly Arg Arg Gly Ile Tyr Arg Phe Val Thr Pro Gly Glu Arg  
 485 490 495  
 Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala  
 500 505 510  
 Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Ser Val Arg Leu  
 515 520 525  
 Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu  
 530 535 540  
 Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His  
 545 550 555 560  
 Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val  
 565 570 575  
 Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser  
 580 585 590  
 Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His  
 595 600 605  
 Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Val  
 610 615 620  
 Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala  
 625 630 635 640  
 Asp Leu Glu Val Val Thr  
 645



## (2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

CGGGGCCTAC TTGGTTGCAT CAAGACTAGC CTTACAGGC

39

## (2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GCCTGTAAGG CTAGTCTTGA TGCAACCAAG TAGGCCCCG

39

## (2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 646 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met	His	Met	His	His	His	His	His	His	Leu	Val	Pro	Arg	Gly	Ser	Ala
1				5					10					15	
Pro	Ile	Thr	Ala	Tyr	Ser	Gln	Gln	Thr	Arg	Gly	Leu	Leu	Gly	Cys	Ile
			20					25					30		
Ile	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val	Glu	Gly	Glu	Val
		35					40					45			
Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala	Thr	Cys	Val	Asn
	50					55						60			

Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser	Lys	Thr	Leu	Ala	
65					70					75					80	
Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	Val	Asp	Gln	Asp	
				85					90					95		
Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	Leu	Thr	Pro	Cys	
			100					105					110			
Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	His	Ala	Asp	Val	
		115					120					125				
Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	Leu	Leu	Ser	Pro	
	130					135						140				
Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ala	Gly	Gly	Pro	Leu	Leu	Cys	
145					150					155					160	
Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	Val	Cys	Thr	Arg	
				165					170					175		
Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	Ser	Met	Glu	Thr	
			180					185					190			
Thr	Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser	Ser	Pro	Pro	Ala	Val	
		195					200					205				
Pro	Gln	Ser	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro	Thr	Gly	Ser	Gly	
	210					215					220					
Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	Gly	Tyr	Lys	Val	
225					230				235						240	
Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly	Phe	Gly	Ala	Tyr	
				245					250					255		
Met	Ser	Lys	Ala	His	Gly	Ile	Asp	Pro	Asn	Ile	Arg	Thr	Gly	Val	Arg	
			260					265					270			
Thr	Ile	Thr	Thr	Gly	Ala	Pro	Val	Thr	Tyr	Ser	Thr	Tyr	Gly	Lys	Phe	
		275					280					285				
Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	Ile	Ile	Ile	Cys	
	290					295					300					
Asp	Glu	Cys	His	Ser	Thr	Asp	Ser	Thr	Thr	Ile	Leu	Gly	Ile	Gly	Thr	
305					310					315					320	
Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	Val	Val	Leu	Ala	
				325					330					335		
Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Val	Pro	His	Pro	Asn	Ile	Glu	
			340					345					350			
Glu	Val	Ala	Leu	Ser	Asn	Thr	Gly	Glu	Ile	Pro	Phe	Tyr	Gly	Lys	Ala	
		355					360					365				

Ile	Pro	Ile	Glu	Ala	Ile	Arg	Gly	Gly	Arg	His	Leu	Ile	Phe	Cys	His	370	375	380
Ser	Lys	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Ala	Lys	Leu	Ser	Gly	Leu	Gly	385	390	395 400
Ile	Asn	Ala	Val	Ala	Tyr	Tyr	Arg	Gly	Leu	Asp	Val	Ser	Val	Ile	Pro	405	410	415
Thr	Ile	Gly	Asp	Val	Val	Val	Val	Ala	Thr	Asp	Ala	Leu	Met	Thr	Gly	420	425	430
Tyr	Thr	Gly	Asp	Phe	Asp	Ser	Val	Ile	Asp	Cys	Asn	Thr	Cys	Val	Thr	435	440	445
Gln	Thr	Val	Asp	Phe	Ser	Leu	Asp	Pro	Thr	Phe	Thr	Ile	Glu	Thr	Thr	450	455	460
Thr	Val	Pro	Gln	Asp	Ala	Val	Ser	Arg	Ser	Gln	Arg	Arg	Gly	Arg	Thr	465	470	475 480
Gly	Arg	Gly	Arg	Arg	Gly	Ile	Tyr	Arg	Phe	Val	Thr	Pro	Gly	Glu	Arg	485	490	495
Pro	Ser	Gly	Met	Phe	Asp	Ser	Ser	Val	Leu	Cys	Glu	Cys	Tyr	Asp	Ala	500	505	510
Gly	Cys	Ala	Trp	Tyr	Glu	Leu	Thr	Pro	Ala	Glu	Thr	Ser	Val	Arg	Leu	515	520	525
Arg	Ala	Tyr	Leu	Asn	Thr	Pro	Gly	Leu	Pro	Val	Cys	Gln	Asp	His	Leu	530	535	540
Glu	Phe	Trp	Glu	Ser	Val	Phe	Thr	Gly	Leu	Thr	His	Ile	Asp	Ala	His	545	550	555 560
Phe	Leu	Ser	Gln	Thr	Lys	Gln	Ala	Gly	Asp	Asn	Phe	Pro	Tyr	Leu	Val	565	570	575
Ala	Tyr	Gln	Ala	Thr	Val	Cys	Ala	Arg	Ala	Gln	Ala	Pro	Pro	Pro	Ser	580	585	590
Trp	Asp	Gln	Met	Trp	Lys	Cys	Leu	Ile	Arg	Leu	Lys	Pro	Thr	Leu	His	595	600	605
Gly	Pro	Thr	Pro	Leu	Leu	Tyr	Arg	Leu	Gly	Ala	Val	Gln	Asn	Glu	Val	610	615	620
Thr	Leu	Thr	His	Pro	Ile	Thr	Lys	Tyr	Ile	Met	Ala	Cys	Met	Ser	Ala	625	630	635 640
Asp	Leu	Glu	Val	Val	Thr											645		

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CTCCTACTTG AAGGGCTCTG CTGGTGGTCC ACTGCTCTGC

40

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 40 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GCAGAGCAGT GGACCACCAG CAGAGCCCTT CAAGTAGGAG

40

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 646 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met	His	Met	His	His	His	His	His	His	Leu	Val	Pro	Arg	Gly	Ser	Ala
1					5				10					15	
Pro	Ile	Thr	Ala	Tyr	Ser	Gln	Gln	Thr	Arg	Gly	Leu	Leu	Gly	Cys	Ile
			20					25					30		
Ile	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val	Glu	Gly	Glu	Val
		35					40					45			
Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala	Thr	Cys	Val	Asn
		50				55					60				
Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser	Lys	Thr	Leu	Ala
65					70					75				80	

115

Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	Val	Asp	Gln	Asp	85	90	95
Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	Leu	Thr	Pro	Cys	100	105	110
Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	His	Ala	Asp	Val	115	120	125
Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	Leu	Leu	Ser	Pro	130	135	140
Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly	Pro	Leu	Leu	Cys	145	150	155
Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	Val	Cys	Thr	Arg	165	170	175
Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	Ser	Met	Glu	Thr	180	185	190
Thr	Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser	Ser	Pro	Pro	Ala	Val	195	200	205
Pro	Gln	Ser	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro	Thr	Gly	Ser	Gly	210	215	220
Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	Gly	Tyr	Lys	Val	225	230	235
Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly	Phe	Gly	Ala	Tyr	245	250	255
Met	Ser	Lys	Ala	His	Gly	Ile	Asp	Pro	Asn	Ile	Arg	Thr	Gly	Val	Arg	260	265	270
Thr	Ile	Thr	Thr	Gly	Ala	Pro	Val	Thr	Tyr	Ser	Thr	Tyr	Gly	Lys	Phe	275	280	285
Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	Ile	Ile	Ile	Cys	290	295	300
Asp	Glu	Cys	His	Ser	Thr	Asp	Ser	Thr	Thr	Ile	Leu	Gly	Ile	Gly	Thr	305	310	315
Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	Val	Val	Leu	Ala	325	330	335
Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Val	Pro	His	Pro	Asn	Ile	Glu	340	345	350
Glu	Val	Ala	Leu	Ser	Asn	Thr	Gly	Glu	Ile	Pro	Phe	Tyr	Gly	Lys	Ala	355	360	365
Ile	Pro	Ile	Glu	Ala	Ile	Arg	Gly	Gly	Arg	His	Leu	Ile	Phe	Cys	His	370	375	380
Ser	Lys	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Ala	Lys	Leu	Ser	Gly	Leu	Gly			

385		390		395		400
Ile Asn Ala Val	Ala Tyr Tyr Arg Gly	Leu Asp Val Ser Val	Ile Pro			
	405	410	415			
Thr Ser Gly Asp	Val Val Val Val	Ala Thr Asp Ala	Leu Met Thr Gly			
	420	425	430			
Tyr Thr Gly Asp	Phe Asp Ser Val	Ile Asp Cys Asn	Thr Cys Val Thr			
	435	440	445			
Gln Thr Val Asp	Phe Ser Leu Asp	Pro Thr Phe Thr	Ile Glu Thr Thr			
	450	455	460			
Thr Val Pro Gln	Asp Ala Val Ser	Arg Ser Gln Arg	Arg Gly Arg Thr			
	465	470	475			480
Gly Arg Gly Arg	Arg Gly Ile Tyr	Arg Phe Val Thr	Pro Gly Glu Arg			
	485	490	495			
Pro Ser Gly Met	Phe Asp Ser Ser	Val Leu Cys Glu	Cys Tyr Asp Ala			
	500	505	510			
Gly Cys Ala Trp	Tyr Glu Leu Thr	Pro Ala Glu Thr	Ser Val Arg Leu			
	515	520	525			
Arg Ala Tyr Leu	Asn Thr Pro Gly	Leu Pro Val Cys	Gln Asp His Leu			
	530	535	540			
Glu Phe Trp Glu	Ser Val Phe Thr	Gly Leu Thr His	Ile Asp Ala His			
	545	550	555			560
Phe Leu Ser Gln	Thr Lys Gln Ala	Gly Asp Asn Phe	Pro Tyr Leu Val			
	565	570	575			
Ala Tyr Gln Ala	Thr Val Cys Ala	Arg Ala Gln Ala	Pro Pro Pro Ser			
	580	585	590			
Trp Asp Gln Met	Trp Lys Cys Leu	Ile Arg Leu Lys	Pro Thr Leu His			
	595	600	605			
Gly Pro Thr Pro	Leu Leu Tyr Arg	Leu Gly Ala Val	Gln Asn Glu Val			
	610	615	620			
Thr Leu Thr His	Pro Ile Thr Lys	Tyr Ile Met Ala	Cys Met Ser Ala			
	625	630	635			640
Asp Leu Glu Val	Val Thr					
	645					

## (2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GTCCGTCATA CCAACTTCCG GAGACGTCGT TGTCG

35

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CGACAACGAC GTCTCCGGAA GTTGGTATGA CGGAC

35

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 646 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Met	His	Met	His	His	His	His	His	His	His	Leu	Val	Pro	Arg	Gly	Ser	Ala
1				5						10					15	
Pro	Ile	Thr	Ala	Tyr	Ser	Gln	Gln	Thr	Arg	Gly	Leu	Leu	Gly	Cys	Ile	
			20					25					30			
Ile	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val	Glu	Gly	Glu	Val	
		35					40					45				
Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala	Thr	Cys	Val	Asn	
		50				55					60					
Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser	Lys	Thr	Leu	Ala	
	65				70				75					80		
Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	Val	Asp	Gln	Asp	
			85						90					95		

Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys  
 100 105 110  
 Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala Asp Val  
 115 120 125  
 Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro  
 130 135 140  
 Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu Leu Cys  
 145 150 155 160  
 Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys Thr Arg  
 165 170 175  
 Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser Met Glu Thr  
 180 185 190  
 Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro Ala Val  
 195 200 205  
 Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro Thr Gly Ser Gly  
 210 215 220  
 Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val  
 225 230 235 240  
 Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr  
 245 250 255  
 Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly Val Arg  
 260 265 270  
 Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly Lys Phe  
 275 280 285  
 Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys  
 290 295 300  
 Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu Gly Ile Gly Thr  
 305 310 315 320  
 Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val Leu Ala  
 325 330 335  
 Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn Ile Glu  
 340 345 350  
 Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala  
 355 360 365  
 Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu Ile Phe Cys His  
 370 375 380  
 Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Ser Gly Leu Gly  
 385 390 395 400  
 Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val Ile Pro



405								410				415			
Thr	Ile	Gly	Asp	Val	Val	Val	Val	Ala	Thr	Asp	Ala	Leu	Met	Thr	Gly
			420							425			430		
Tyr	Thr	Gly	Asp	Phe	Asp	Ser	Val	Ile	Asp	Cys	Asn	Thr	Cys	Val	Thr
		435					440					445			
Gln	Thr	Val	Asp	Phe	Ser	Leu	Asp	Pro	Thr	Phe	Thr	Ile	Glu	Thr	Thr
		450				455						460			
Thr	Val	Pro	Gln	Asp	Ala	Val	Ser	Arg	Ser	Gln	Arg	Arg	Gly	Arg	Thr
465					470					475					480
Gly	Arg	Gly	Arg	Arg	Gly	Ile	Tyr	Arg	Phe	Val	Thr	Pro	Gly	Glu	Arg
				485					490					495	
Pro	Ser	Gly	Met	Phe	Asp	Ser	Ser	Val	Leu	Cys	Glu	Cys	Tyr	Asp	Ala
			500						505				510		
Gly	Cys	Ala	Trp	Tyr	Glu	Leu	Thr	Pro	Ala	Glu	Thr	Ser	Val	Arg	Leu
		515					520					525			
Arg	Ala	Tyr	Leu	Asn	Thr	Pro	Gly	Leu	Pro	Val	Cys	Gln	Asp	His	Leu
		530				535					540				
Glu	Phe	Trp	Glu	Ser	Val	Phe	Thr	Gly	Leu	Thr	His	Ile	Asp	Ala	His
545					550					555					560
Phe	Leu	Ser	Gln	Thr	Lys	Gln	Ala	Gly	Asp	Asn	Phe	Pro	Tyr	Leu	Val
				565					570					575	
Ala	Tyr	Gln	Ala	Thr	Val	Cys	Ala	Arg	Ala	Gln	Ala	Pro	Pro	Pro	Ser
			580						585				590		
Trp	Asp	Gln	Met	Trp	Lys	Cys	Leu	Ile	Arg	Leu	Lys	Pro	Thr	Leu	His
		595					600					605			
Gly	Pro	Thr	Pro	Leu	Leu	Tyr	Arg	Leu	Gly	Ala	Val	Gln	Asn	Glu	Val
	610					615					620				
Thr	Leu	Thr	His	Pro	Ile	Thr	Lys	Tyr	Ile	Met	Ala	Cys	Met	Ser	Ala
625					630					635					640
Asp	Leu	Glu	Val	Val	Thr										
				645											

## (2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:  
ACTAAAGTGC CGGCTGCCTA CGCAGCCCAA GGG 33

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:  
CCCTTGGGCT GCGTAGGCAG CCGGCACTTT AGT 33

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:  
CGGGGCCTAC TTGGTTGCAA GATCACTAGC CTTACAGGC 39

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:  
GCCTGTAAGG CTAGTGATCT TGCAACCAAG TAGGCCCCG 39

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CGGGGCCTAC TTGGTTGCAT CAAGACTAGC CTTACAGGC

39

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GCCTGTAAGG CTAGTCTTGA TGCAACCAAG TAGGCCCCG

39

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CGGGGCCTAC TTGGTTGCAA GAAGACTAGC CTTACAGG

38

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

122

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GCCTGTAAGG CTAGTCTTCT TGCAACCAAG TAGGCCCCG

39

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

CGGGGCCTAC TTGGTTGCAA GATCACTAGC CTTACAGGC

39

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GCCTGTAAGG CTAGTGATCT TGCAACCAAG TAGGCCCCG

39

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

CGGGGCCTAC TTGGTTGCAT CAAGACTAGC CTTACAGGC

39

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GCCTGTAAGG CTAGTCTTGA TGCAACCAAG TAGGCCCCG

39

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

CGGGGCCTAC TTGGTTGCAA GAAGACTAGC CTTACAGGC

39

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GCCTGTAAGG CTAGTCTTCT TGCAACCAAG TAGGCCCCG

39

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 96 base pairs
  - (B) TYPE: nucleic acid

124

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GATATACATA TGGCTTACTC TCTGACTACG GGTTCGTGTG TTATTGTTGG TAGAATTATT 60  
TTATCTGGTA GTGGTAGTAT CACGGCCTAC TCCCAA 96

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 51 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GTGGTGGTGC TCGAGGCTGC CGCGCGGCAC CAGCGTAACG ACCTCCAGGT C 51

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 96 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GATATACATA TGGCTTACTC TCTGACTACG GGTTCGTGTG TTATTGTTGG TAGAATTATT 60  
TTATCTGGTA GTGGTAGTAT CACGGCCTAC TCCCAA 96

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

TGGTGGTGCT CGAGGCTGCC GCGCGGCACC AGCGTAACGA CCTCCAGGTC

50

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Asp Thr Glu Asp Val Val Ala Cys Ser Met Ser Tyr Thr Trp Tyr Gly  
1                      5                      10                      15

Lys

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG                      48  
Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro  
1                      5                      10                      15

CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA                      96  
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu  
20                      25                      30

TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA                      144  
Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu

126

35					40					45						
CTT	GGT	TGC	ATC	ATC	ACT	AGC	CTT	ACA	GGC	CGG	GAC	AAG	AAC	CAG	GTC	192
Leu	Gly	Cys	Ile	Ile	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val	
50					55					60						
GAG	GGA	GAG	GTT	CAG	GTG	GTT	TCC	ACC	GCA	ACA	CAA	TCC	TTC	CTG	GCG	240
Glu	Gly	Glu	Val	Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala	
65					70					75					80	
ACC	TGC	GTC	AAC	GGC	GTG	TGT	TGG	ACC	GTT	TAC	CAT	GGT	GCT	GGC	TCA	288
Thr	Cys	Val	Asn	Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser	
85					90					95						
AAG	ACC	TTA	GCC	GGC	CCA	AAG	GGG	CCA	ATC	ACC	CAG	ATG	TAC	ACT	AAT	336
Lys	Thr	Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	
100					105					110						
GTG	GAC	CAG	GAC	CTC	GTC	GGC	TGG	CAG	GCG	CCC	CCC	GGG	GCG	CGT	TCC	384
Val	Asp	Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	
115					120					125						
TTG	ACA	CCA	TGC	ACC	TGT	GGC	AGC	TCA	GAC	CTT	TAC	TTG	GTC	ACG	AGA	432
Leu	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	
130					135					140						
CAT	GCT	GAC	GTC	ATT	CCG	GTG	CGC	CGG	CGG	GGC	GAC	AGT	AGG	GGG	AGC	480
His	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	
145					150					155					160	
CTG	CTC	TCC	CCC	AGG	CCT	GTC	TCC	TAC	TTG	AAG	GGC	TCT	TCG	GGT	GGT	528
Leu	Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly	
165					170					175						
CCA	CTG	CTC	TGC	CCT	TCG	GGG	CAC	GCT	GTG	GGC	ATC	TTC	CGG	GCT	GCC	576
Pro	Leu	Leu	Cys	Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	
180					185					190						
GTA	TGC	ACC	CGG	GGG	GTT	GCG	AAG	GCG	GTG	GAC	TTT	GTG	CCC	GTA	GAG	624
Val	Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	
195					200					205						
TCC	ATG	GAA	ACT	ACT	ATG	CGG	TCT	TGA								651
Ser	Met	Glu	Thr	Thr	Met	Arg	Ser									
210					215											

## (2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 651 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

127



## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..651

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG	48
Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro	
1 5 10 15	
CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA	96
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	
20 25 30	
TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA	144
Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu	
35 40 45	
CTT GGT TGC AAG ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC	192
Leu Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val	
50 55 60	
GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG	240
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala	
65 70 75 80	
ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA	288
Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser	
85 90 95	
AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT	336
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn	
100 105 110	
GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC	384
Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser	
115 120 125	
TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA	432
Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg	
130 135 140	
CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC	480
His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser	
145 150 155 160	
CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT	528
Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly	
165 170 175	
CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC	576
Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala	
180 185 190	
GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG	624
Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu	
195 200 205	

TCC ATG GAA ACT ACT ATG CGG TCT TGA  
 Ser Met Glu Thr Thr Met Arg Ser  
 210 215

651

## (2) INFORMATION FOR SEQ ID NO:94:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..651

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG	48
Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro	
1 5 10 15	
CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA	96
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	
20 25 30	
TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA	144
Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu	
35 40 45	
CTT GGT TGC ATC AAG ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC	192
Leu Gly Cys Ile Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val	
50 55 60	
GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG	240
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala	
65 70 75 80	
ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA	288
Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser	
85 90 95	
AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT	336
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn	
100 105 110	
GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC	384
Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser	
115 120 125	
TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA	432
Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg	
130 135 140	

129

[illegible]

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 1..651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

ATG	GGC	AGC	AGC	CAT	CAT	CAT	CAT	CAT	CAC	AGC	AGC	GGC	CTG	GTG	CCG	48
Met	Gly	Ser	Ser	His	His	His	His	His	His	Ser	Ser	Gly	Leu	Val	Pro	
1				5					10					15		
CGC	GGC	AGC	CAT	ATG	GGT	TCT	GTT	GTT	ATT	GTT	GGT	AGA	ATT	ATT	TTA	96
Arg	Gly	Ser	His	Met	Gly	Ser	Val	Val	Ile	Val	Gly	Arg	Ile	Ile	Leu	
			20					25					30			
TCT	GGT	AGT	GGT	AGT	ATC	ACG	GCC	TAC	TCC	CAA	CAG	ACG	CGG	GGC	CTA	144
Ser	Gly	Ser	Gly	Ser	Ile	Thr	Ala	Tyr	Ser	Gln	Gln	Thr	Arg	Gly	Leu	
		35					40					45				
CTT	GGT	TGC	AAG	AAG	ACT	AGC	CTT	ACA	GGC	CGG	GAC	AAG	AAC	CAG	GTC	192
Leu	Gly	Cys	Lys	Lys	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val	
	50					55				60						
GAG	GGA	GAG	GTT	CAG	GTG	GTT	TCC	ACC	GCA	ACA	CAA	TCC	TTC	CTG	GCG	240

130

Glu	Gly	Glu	Val	Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala			
65					70					75					80			
ACC	TGC	GTC	AAC	GGC	GTG	TGT	TGG	ACC	GTT	TAC	CAT	GGT	GCT	GGC	TCA		288	
Thr	Cys	Val	Asn	Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser			
				85					90					95				
AAG	ACC	TTA	GCC	GGC	CCA	AAG	GGG	CCA	ATC	ACC	CAG	ATG	TAC	ACT	AAT		336	
Lys	Thr	Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn			
			100					105					110					
GTG	GAC	CAG	GAC	CTC	GTC	GGC	TGG	CAG	GCG	CCC	CCC	GGG	GCG	CGT	TCC		384	
Val	Asp	Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser			
		115					120					125						
TTG	ACA	CCA	TGC	ACC	TGT	GGC	AGC	TCA	GAC	CTT	TAC	TTG	GTC	ACG	AGA		432	
Leu	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg			
	130					135					140							
CAT	GCT	GAC	GTC	ATT	CCG	GTG	CGC	CGG	CGG	GGC	GAC	AGT	AGG	GGG	AGC		480	
His	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser			
145					150					155					160			
CTG	CTC	TCC	CCC	AGG	CCT	GTC	TCC	TAC	TTG	AAG	GGC	TCT	TCG	GGT	GGT		528	
Leu	Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly			
				165					170					175				
CCA	CTG	CTC	TGC	CCT	TCG	GGG	CAC	GCT	GTG	GGC	ATC	TTC	CGG	GCT	GCC		576	
Pro	Leu	Leu	Cys	Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala			
			180					185					190					
GTA	TGC	ACC	CGG	GGG	GTT	GCG	AAG	GCG	GTG	GAC	TTT	GTG	CCC	GTA	GAG		624	
Val	Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu			
		195					200					205						
TCC	ATG	GAA	ACT	ACT	ATG	CGG	TCT	TGA									651	
Ser	Met	Glu	Thr	Thr	Met	Arg	Ser											
	210					215												

## (2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 651 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
- (A) NAME/KEY: CDS
  - (B) LOCATION: 1..651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG	48
Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro	
1 5 10 15	
CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA	96
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	
20 25 30	
TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA	144
Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu	
35 40 45	
CTT GGT TGC ATC ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC	192
Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val	
50 55 60	
GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG	240
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala	
65 70 75 80	
ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA	288
Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser	
85 90 95	
AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT	336
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn	
100 105 110	
GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC	384
Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser	
115 120 125	
TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA	432
Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg	
130 135 140	
CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC	480
His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser	
145 150 155 160	
CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT GCT GGT GGT	528
Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly	
165 170 175	
CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC	576
Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala	
180 185 190	
GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG	624
Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu	
195 200 205	
TCC ATG GAA ACT ACT ATG CGG TCT TGA	651
Ser Met Glu Thr Thr Met Arg Ser	
210 215	

(2) INFORMATION FOR SEQ ID NO:97:

132

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 651 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG	48
Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro	
1 5 10 15	
CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA	96
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	
20 25 30	
TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA	144
Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu	
35 40 45	
CTT GGT TGC AAG ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC	192
Leu Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val	
50 55 60	
GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG	240
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala	
65 70 75 80	
ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA	288
Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser	
85 90 95	
AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT	336
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn	
100 105 110	
GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC	384
Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser	
115 120 125	
TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA	432
Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg	
130 135 140	
CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC	480
His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser	
145 150 155 160	
CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT GCT GGT GGT	528

Leu	Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ala	Gly	Gly	
				165					170					175		
CCA	CTG	CTC	TGC	CCT	TCG	GGG	CAC	GCT	GTG	GGC	ATC	TTC	CGG	GCT	GCC	576
Pro	Leu	Leu	Cys	Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	
			180					185					190			
GTA	TGC	ACC	CGG	GGG	GTT	GCG	AAG	GCG	GTG	GAC	TTT	GTG	CCC	GTA	GAG	624
Val	Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	
		195					200					205				
TCC	ATG	GAA	ACT	ACT	ATG	CGG	TCT	TGA								651
Ser	Met	Glu	Thr	Thr	Met	Arg	Ser									
	210					215										

## (2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 651 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
- (A) NAME/KEY: CDS
  - (B) LOCATION: 1..651

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

ATG	GGC	AGC	AGC	CAT	CAT	CAT	CAT	CAT	CAC	AGC	AGC	GGC	CTG	GTG	CCG	48
Met	Gly	Ser	Ser	His	His	His	His	His	His	Ser	Ser	Gly	Leu	Val	Pro	
1				5					10					15		
CGC	GGC	AGC	CAT	ATG	GGT	TCT	GTT	GTT	ATT	GTT	GGT	AGA	ATT	ATT	TTA	96
Arg	Gly	Ser	His	Met	Gly	Ser	Val	Val	Ile	Val	Gly	Arg	Ile	Ile	Leu	
			20					25					30			
TCT	GGT	AGT	GGT	AGT	ATC	ACG	GCC	TAC	TCC	CAA	CAG	ACG	CGG	GGC	CTA	144
Ser	Gly	Ser	Gly	Ser	Ile	Thr	Ala	Tyr	Ser	Gln	Gln	Thr	Arg	Gly	Leu	
		35				40						45				
CTT	GGT	TGC	ATC	AAG	ACT	AGC	CTT	ACA	GGC	CGG	GAC	AAG	AAC	CAG	GTC	192
Leu	Gly	Cys	Ile	Lys	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val	
	50					55				60						
GAG	GGA	GAG	GTT	CAG	GTG	GTT	TCC	ACC	GCA	ACA	CAA	TCC	TTC	CTG	GCG	240
Glu	Gly	Glu	Val	Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala	
	65				70				75					80		
ACC	TGC	GTC	AAC	GGC	GTG	TGT	TGG	ACC	GTT	TAC	CAT	GGT	GCT	GGC	TCA	288
Thr	Cys	Val	Asn	Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser	
			85						90					95		

AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT	336
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn	
100 105 110	
GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC	384
Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser	
115 120 125	
TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA	432
Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg	
130 135 140	
CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC	480
His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser	
145 150 155 160	
CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT GCT GGT GGT	528
Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly	
165 170 175	
CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC	576
Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala	
180 185 190	
GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG	624
Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu	
195 200 205	
TCC ATG GAA ACT ACT ATG CGG TCT TGA	651
Ser Met Glu Thr Thr Met Arg Ser	
210 215	

## (2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 651 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..651

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG	48
Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro	
1 5 10 15	
CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA	96
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	

135



20	25	30	
TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu 35 40 45			144
CTT GGT TGC AAG AAG ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC Leu Gly Cys Lys Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val 50 55 60			192
GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala 65 70 75 80			240
ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser 85 90 95			288
AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn 100 105 110			336
GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser 115 120 125			384
TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg 130 135 140			432
CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser 145 150 155 160			480
CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT GCT GGT GGT Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly 165 170 175			528
CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala 180 185 190			576
GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu 195 200 205			624
TCC ATG GAA ACT ACT ATG CGG TCT TGA Ser Met Glu Thr Thr Met Arg Ser 210 215			651

## (2) INFORMATION FOR SEQ ID NO:100:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

136

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG	48
Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro	
1 5 10 15	
CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA	96
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	
20 25 30	
TCT CCT GCT GGT GGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA	144
Ser Pro Ala Gly Gly Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu	
35 40 45	
CTT GGT TGC ATC ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC	192
Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val	
50 55 60	
GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG	240
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala	
65 70 75 80	
ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA	288
Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser	
85 90 95	
AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT	336
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn	
100 105 110	
GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC	384
Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser	
115 120 125	
TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA	432
Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg	
130 135 140	
CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC	480
His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser	
145 150 155 160	
CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT	528
Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly	
165 170 175	
CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC	576
Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala	
180 185 190	

GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG	624
Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu	
195 200 205	

TCC ATG GAA ACT ACT ATG CGG TCT TGA	651
Ser Met Glu Thr Thr Met Arg Ser	
210 215	

## (2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 651 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
- (A) NAME/KEY: CDS
  - (B) LOCATION: 1..651

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG	48
Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro	
1 5 10 15	
CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA	96
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	
20 25 30	
TCT CCT GCT GGT GGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA	144
Ser Pro Ala Gly Gly Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu	
35 40 45	
CTT GGT TGC AAG ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC	192
Leu Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val	
50 55 60	
GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG	240
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala	
65 70 75 80	
ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA	288
Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser	
85 90 95	
AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT	336
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn	
100 105 110	
GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC	384
Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser	

CTT	GGT	TGC	ATC	ATC	ACT	AGC	CTT	ACA	GGC	CGG	GAC	AAG	AAC	CAG	GTC	192
Leu	Gly	Cys	Ile	Ile	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val	
	50					55					60					
GAG	GGA	GAG	GTT	CAG	GTG	GTT	TCC	ACC	GCA	ACA	CAA	TCC	TTC	CTG	GCG	240
Glu	Gly	Glu	Val	Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala	
	65				70					75					80	
ACC	TGC	GTC	AAC	GGC	GTG	TGT	TGG	ACC	GTT	TAC	CAT	GGT	GCT	GGC	TCA	288
Thr	Cys	Val	Asn	Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser	
				85					90					95		
AAG	ACC	TTA	GCC	GGC	CCA	AAG	GGG	CCA	ATC	ACC	CAG	ATG	TAC	ACT	AAT	336
Lys	Thr	Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	
			100					105					110			
GTG	GAC	CAG	GAC	CTC	GTC	GGC	TGG	CAG	GCG	CCC	CCC	GGG	GCG	CGT	TCC	384
Val	Asp	Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	
		115					120					125				
TTG	ACA	CCA	TGC	ACC	TGT	GGC	AGC	TCA	GAC	CTT	TAC	TTG	GTC	ACG	AGA	432
Leu	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	
	130					135					140					
CAT	GCT	GAC	GTC	ATT	CCG	GTG	CGC	CGG	CGG	GGC	GAC	AGT	AGG	GGG	AGC	480
His	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	
	145				150					155					160	
CTG	CTC	TCC	CCC	AGG	CCT	GTC	TCC	TAC	TTG	AAG	GGC	TCT	TCG	GGT	GGT	528
Leu	Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly	
				165					170					175		
CCA	CTG	CTC	TGC	CCT	TCG	GGG	CAC	GCT	GTG	GGC	ATC	TTC	CGG	GCT	GCC	576
Pro	Leu	Leu	Cys	Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	
			180					185					190			
GTA	TGC	ACC	CGG	GGG	GTT	GCG	AAG	GCG	GTG	GAC	TTT	GTG	CCC	GTA	GAG	624
Val	Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	
		195					200					205				
TCC	ATG	GAA	ACT	ACT	ATG	CGG	TCT	CCG	GTC	TTC	ACG	GAC	AAC	TCA	TCC	672
Ser	Met	Glu	Thr	Thr	Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser	Ser	
	210					215					220					
CCC	CCG	GCC	GTA	CCG	CAG	TCA	TTT	CAA	GTG	GCC	CAC	CTA	CAC	GCT	CCC	720
Pro	Pro	Ala	Val	Pro	Gln	Ser	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro	
	225				230					235					240	
ACT	GGC	AGC	GGC	AAG	AGT	ACT	AAA	GTG	CCG	GCT	GCA	TAT	GCA	GCC	CAA	768
Thr	Gly	Ser	Gly	Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	
				245				250						255		
GGG	TAC	AAG	GTG	CTC	GTC	CTC	AAT	CCG	TCC	GTT	GCC	GCT	ACC	TTA	GGG	816
Gly	Tyr	Lys	Val	Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly	
			260					265					270			
TTT	GGG	GCG	TAT	ATG	TCT	AAG	GCA	CAC	GGT	ATT	GAC	CCC	AAC	ATC	AGA	864
Phe	Gly	Ala	Tyr	Met	Ser	Lys	Ala	His	Gly	Ile	Asp	Pro	Asn	Ile	Arg	

115	120	125	
TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA			432
Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg			
130	135	140	
CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC			480
His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser			
145	150	155	160
CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT			528
Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly			
	165	170	175
CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC			576
Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala			
	180	185	190
GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG			624
Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu			
	195	200	205
TCC ATG GAA ACT ACT ATG CGG TCT TGA			651
Ser Met Glu Thr Thr Met Arg Ser			
210	215		

## (2) INFORMATION FOR SEQ ID NO:102:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1998

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG	48
Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro	
1 5 10 15	
CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA	96
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	
20 25 30	
TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA	144
Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu	
35 40 45	

275	280	285	
ACT GGG GTA AGG ACC ATT ACC ACA GGC GCC CCC GTC ACA TAC TCT ACC Thr Gly Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr 290 295 300			912
TAT GGC AAG TTT CTT GCC GAT GGT GGT TGC TCT GGG GGC GCT TAT GAC Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp 305 310 315 320			960
ATC ATA ATA TGT GAT GAG TGC CAT TCA ACT GAC TCG ACT ACA ATC TTG Ile Ile Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu 325 330 335			1008
GGC ATC GGC ACA GTC CTG GAC CAA GCG GAG ACG GCT GGA GCG CGG CTT Gly Ile Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu 340 345 350			1056
GTC GTG CTC GCC ACC GCT ACG CCT CCG GGA TCG GTC ACC GTG CCA CAC Val Val Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His 355 360 365			1104
CCA AAC ATC GAG GAG GTG GCC CTG TCT AAT ACT GGA GAG ATC CCC TTC Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe 370 375 380			1152
TAT GGC AAA GCC ATC CCC ATT GAA GCC ATC AGG GGG GGA AGG CAT CTC Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu 385 390 395 400			1200
ATT TTC TGT CAT TCC AAG AAG AAG TGC GAC GAG CTC GCC GCA AAG CTG Ile Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu 405 410 415			1248
TCA GGC CTC GGA ATC AAC GCT GTG GCG TAT TAC CGG GGG CTC GAT GTG Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val 420 425 430			1296
TCC GTC ATA CCA ACT ATC GGA GAC GTC GTT GTC GTG GCA ACA GAC GCT Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala 435 440 445			1344
CTG ATG ACG GGC TAT ACG GGC GAC TTT GAC TCA GTG ATC GAC TGT AAC Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn 450 455 460			1392
ACA TGT GTC ACC CAG ACA GTC GAC TTC AGC TTG GAT CCC ACC TTC ACC Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr 465 470 475 480			1440
ATT GAG ACG ACG ACC GTG CCT CAA GAC GCA GTG TCG CGC TCG CAG CGG Ile Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg 485 490 495			1488
CGG GGT AGG ACT GGC AGG GGT AGG AGA GGC ATC TAC AGG TTT GTG ACT Arg Gly Arg Thr Gly Arg Gly Arg Arg Gly Ile Tyr Arg Phe Val Thr 500 505 510			1536

CCG GGA GAA CGG CCC TCG GGC ATG TTC GAT TCC TCG GTC CTG TGT GAG	1584
Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu	
515 520 525	
TGC TAT GAC GCG GGC TGT GCT TGG TAC GAG CTC ACC CCC GCC GAG ACC	1632
Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr	
530 535 540	
TCG GTT AGG TTG CGG GCC TAC CTG AAC ACA CCA GGG TTG CCC GTT TGC	1680
Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys	
545 550 555 560	
CAG GAC CAC CTG GAG TTC TGG GAG AGT GTC TTC ACA GGC CTC ACC CAT	1728
Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His	
565 570 575	
ATA GAT GCA CAC TTC TTG TCC CAG ACC AAG CAG GCA GGA GAC AAC TTC	1776
Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe	
580 585 590	
CCC TAC CTG GTA GCA TAC CAA GCC ACG GTG TGC GCC AGG GCT CAG GCC	1824
Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala	
595 600 605	
CCA CCT CCA TCA TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA	1872
Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys	
610 615 620	
CCT ACG CTG CAC GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC	1920
Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val	
625 630 635 640	
CAA AAT GAG GTC ACC CTC ACC CAC CCC ATA ACC AAA TAC ATC ATG GCA	1968
Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala	
645 650 655	
TGC ATG TCG GCT GAC CTG GAG GTC GTC ACT	1998
Cys Met Ser Ala Asp Leu Glu Val Val Thr	
660 665	

## (2) INFORMATION FOR SEQ ID NO:103:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1998

142

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG	48
Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro	
1 5 10 15	
CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA	96
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	
20 25 30	
TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA	144
Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu	
35 40 45	
CTT GGT TGC AAG ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC	192
Leu Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val	
50 55 60	
GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG	240
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala	
65 70 75 80	
ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA	288
Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser	
85 90 95	
AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT	336
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn	
100 105 110	
GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC	384
Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser	
115 120 125	
TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA	432
Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg	
130 135 140	
CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC	480
His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser	
145 150 155 160	
CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT	528
Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly	
165 170 175	
CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC	576
Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala	
180 185 190	
GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG	624
Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu	
195 200 205	
TCC ATG GAA ACT ACT ATG CGG TCT CCG GTC TTC ACG GAC AAC TCA TCC	672
Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser	
210 215 220	



CCC Pro 225	CCG Pro 225	GCC Ala 225	GTA Val 225	CCG Pro 225	CAG Gln 230	TCA Ser 230	TTT Phe 230	CAA Gln 235	GTG Val 235	GCC Ala 235	CAC His 235	CTA Leu 235	CAC His 235	GCT Ala 240	CCC Pro 240	720
ACT Thr 245	GGC Gly 245	AGC Ser 245	GGC Gly 245	AAG Lys 245	AGT Ser 245	ACT Thr 245	AAA Lys 245	GTG Val 250	CCG Pro 250	GCT Ala 250	GCA Ala 250	TAT Tyr 250	GCA Ala 255	GCC Ala 255	CAA Gln 255	768
GGG Gly 260	TAC Tyr 260	AAG Lys 260	GTG Val 260	CTC Leu 260	GTC Val 260	CTC Leu 265	AAT Asn 265	CCG Pro 265	TCC Ser 265	GTT Val 265	GCC Ala 265	GCT Ala 270	ACC Thr 270	TTA Leu 270	GGG Gly 270	816
TTT Phe 275	GGG Gly 275	GCG Ala 275	TAT Tyr 275	ATG Met 275	TCT Ser 275	AAG Lys 280	GCA Ala 280	CAC His 280	GGT Gly 280	ATT Ile 280	GAC Asp 285	CCC Pro 285	AAC Asn 285	ATC Ile 285	AGA Arg 285	864
ACT Thr 290	GGG Gly 290	GTA Val 290	AGG Arg 290	ACC Thr 290	ATT Ile 295	ACC Thr 295	ACA Thr 295	GGC Gly 295	GCC Ala 295	CCC Pro 300	GTC Val 300	ACA Thr 300	TAC Tyr 300	TCT Ser 300	ACC Thr 300	912
TAT Tyr 305	GGC Gly 305	AAG Lys 305	TTT Phe 305	CTT Leu 310	GCC Ala 310	GAT Asp 310	GGT Gly 310	GGT Gly 315	TGC Cys 315	TCT Ser 315	GGG Gly 315	GGC Gly 315	GCT Ala 320	TAT Tyr 320	GAC Asp 320	960
ATC Ile 325	ATA Ile 325	ATA Ile 325	TGT Cys 325	GAT Asp 325	GAG Glu 325	TGC Cys 325	CAT His 325	TCA Ser 330	ACT Thr 330	GAC Asp 330	TCG Ser 330	ACT Thr 330	ACA Thr 335	ATC Ile 335	TTG Leu 335	1008
GGC Gly 340	ATC Ile 340	GGC Gly 340	ACA Thr 340	GTC Val 340	CTG Leu 340	GAC Asp 345	CAA Gln 345	GCG Ala 345	GAG Glu 345	ACG Thr 345	GCT Ala 350	GGA Gly 350	GCG Ala 350	CGG Arg 350	CTT Leu 350	1056
GTC Val 355	GTG Val 355	CTC Leu 355	GCC Ala 355	ACC Thr 355	GCT Ala 360	ACG Thr 360	CCT Pro 360	CCG Pro 360	GGA Gly 365	TCG Ser 365	GTC Val 365	ACC Thr 365	GTG Val 365	CCA Pro 365	CAC His 365	1104
CCA Pro 370	AAC Asn 370	ATC Ile 370	GAG Glu 370	GAG Glu 370	GTG Val 375	GCC Ala 375	CTG Leu 375	TCT Ser 375	AAT Asn 375	ACT Thr 375	GGA Gly 380	GAG Glu 380	ATC Ile 380	CCC Pro 380	TTC Phe 380	1152
TAT Tyr 385	GGC Gly 385	AAA Lys 385	GCC Ala 385	ATC Ile 385	CCC Pro 390	ATT Ile 390	GAA Glu 390	GCC Ala 390	ATC Ile 395	AGG Arg 395	GGG Gly 395	GGA Gly 395	AGG Arg 395	CAT His 395	CTC Leu 400	1200
ATT Ile 405	TTC Phe 405	TGT Cys 405	CAT His 405	TCC Ser 405	AAG Lys 405	AAG Lys 405	AAG Lys 405	TGC Cys 410	GAC Asp 410	GAG Glu 410	CTC Leu 410	GCC Ala 410	GCA Ala 415	AAG Lys 415	CTG Leu 415	1248
TCA Ser 420	GGC Gly 420	CTC Leu 420	GGA Gly 420	ATC Ile 420	AAC Asn 425	GCT Ala 425	GTG Val 425	GCG Ala 425	TAT Tyr 425	TAC Tyr 425	CGG Arg 430	GGG Gly 430	CTC Leu 430	GAT Asp 430	GTG Val 430	1296
TCC Ser 435	GTC Val 435	ATA Ile 435	CCA Pro 435	ACT Thr 435	ATC Ile 440	GGA Gly 440	GAC Asp 440	GTC Val 440	GTT Val 440	GTC Val 445	GTG Val 445	GCA Ala 445	ACA Thr 445	GAC Asp 445	GCT Ala 445	1344
CTG Leu 1392	ATG Met 1392	ACG Thr 1392	GGC Gly 1392	TAT Tyr 1392	ACG Thr 1392	GGC Gly 1392	GAC Asp 1392	TTT Phe 1392	GAC Asp 1392	TCA Ser 1392	GTG Val 1392	ATC Ile 1392	GAC Asp 1392	TGT Cys 1392	AAC Asn 1392	1392

450	455	460	
ACA TGT GTC ACC CAG Thr Cys Val Thr Gln 465	ACA GTC GAC TTC AGC Thr Val Asp Phe Ser 470	TTG GAT CCC ACC TTC ACC Leu Asp Pro Thr Phe Thr 475	1440
ATT GAG ACG ACG ACC Ile Glu Thr Thr Thr 485	GTG CCT CAA GAC GCA Val Pro Gln Asp Ala 490	GTG TCG CGC TCG CAG CGG Val Ser Arg Ser Gln Arg 495	1488
CGG GGT AGG ACT GGC Arg Gly Arg Thr Gly 500	AGG GGT AGG AGA GGC Arg Gly Arg Arg Gly 505	ATC TAC AGG TTT GTG ACT Ile Tyr Arg Phe Val Thr 510	1536
CCG GGA GAA CGG CCC Pro Gly Glu Arg Pro 515	TCG GGC ATG TTC GAT Ser Gly Met Phe Asp 520	TCC TCG GTC CTG TGT GAG Ser Ser Val Leu Cys Glu 525	1584
TGC TAT GAC GCG GGC Cys Tyr Asp Ala Gly 530	TGT GCT TGG TAC GAG Cys Ala Trp Tyr Glu 535	CTC ACC CCC GCC GAG ACC Leu Thr Pro Ala Glu Thr 540	1632
TCG GTT AGG TTG CGG Ser Val Arg Leu Arg 545	GCC TAC CTG AAC ACA Ala Tyr Leu Asn Thr 550	CCA GGG TTG CCC GTT TGC Pro Gly Leu Pro Val Cys 555	1680
CAG GAC CAC CTG GAG Gln Asp His Leu Glu 565	TTC TGG GAG AGT GTC Phe Trp Glu Ser Val 570	TTC ACA GGC CTC ACC CAT Phe Thr Gly Leu Thr His 575	1728
ATA GAT GCA CAC TTC Ile Asp Ala His Phe 580	TTG TCC CAG ACC AAG Leu Ser Gln Thr Lys 585	CAG GCA GGA GAC AAC TTC Gln Ala Gly Asp Asn Phe 590	1776
CCC TAC CTG GTA GCA Pro Tyr Leu Val Ala 595	TAC CAA GCC ACG GTG Tyr Gln Ala Thr Val 600	TGC GCC AGG GCT CAG GCC Cys Ala Arg Ala Gln Ala 605	1824
CCA CCT CCA TCA TGG Pro Pro Ser Trp Asp 610	CAA ATG TGG AAG TGT Gln Met Trp Lys Cys 615	CTC ATA CGG CTG AAA Leu Ile Arg Leu Lys 620	1872
CCT ACG CTG CAC GGG Pro Thr Leu His Gly 625	CCA ACA CCC TTG CTG Pro Thr Pro Leu Leu 630	TAC AGG CTG GGA GCC GTC Tyr Arg Leu Gly Ala Val 635	1920
CAA AAT GAG GTC ACC Gln Asn Glu Val Thr 645	CTC ACC CAC CCC ATA Leu Thr His Pro Ile 650	ACC AAA TAC ATC ATG GCA Thr Lys Tyr Ile Met Ala 655	1968
TGC ATG TCG GCT GAC Cys Met Ser Ala Asp 660	CTG GAG GTC GTC ACT Leu Glu Val Val Thr 665		1998

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

145

- (A) LENGTH: 1998 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..1998

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG	48
Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro	
1 5 10 15	
CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA	96
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	
20 25 30	
TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA	144
Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu	
35 40 45	
CTT GGT TGC ATC AAG ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC	192
Leu Gly Cys Ile Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val	
50 55 60	
GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG	240
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala	
65 70 75 80	
ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA	288
Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser	
85 90 95	
AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT	336
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn	
100 105 110	
GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC	384
Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser	
115 120 125	
TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA	432
Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg	
130 135 140	
CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC	480
His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser	
145 150 155 160	
CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT	528
Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly	

176

147

ATT	TTC	TGT	CAT	TCC	AAG	AAG	AAG	TGC	GAC	GAG	CTC	GCC	GCA	AAG	CTG	1248
Ile	Phe	Cys	His	Ser	Lys	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Ala	Lys	Leu	
				405					410					415		
TCA	GGC	CTC	GGA	ATC	AAC	GCT	GTG	GCG	TAT	TAC	CGG	GGG	CTC	GAT	GTG	1296
Ser	Gly	Leu	Gly	Ile	Asn	Ala	Val	Ala	Tyr	Tyr	Arg	Gly	Leu	Asp	Val	
			420					425					430			
TCC	GTC	ATA	CCA	ACT	ATC	GGA	GAC	GTC	GTT	GTC	GTG	GCA	ACA	GAC	GCT	1344
Ser	Val	Ile	Pro	Thr	Ile	Gly	Asp	Val	Val	Val	Val	Ala	Thr	Asp	Ala	
		435					440					445				
CTG	ATG	ACG	GGC	TAT	ACG	GGC	GAC	TTT	GAC	TCA	GTG	ATC	GAC	TGT	AAC	1392
Leu	Met	Thr	Gly	Tyr	Thr	Gly	Asp	Phe	Asp	Ser	Val	Ile	Asp	Cys	Asn	
	450					455					460					
ACA	TGT	GTC	ACC	CAG	ACA	GTC	GAC	TTC	AGC	TTG	GAT	CCC	ACC	TTC	ACC	1440
Thr	Cys	Val	Thr	Gln	Thr	Val	Asp	Phe	Ser	Leu	Asp	Pro	Thr	Phe	Thr	
465					470					475					480	
ATT	GAG	ACG	ACG	ACC	GTG	CCT	CAA	GAC	GCA	GTG	TCG	CGC	TCG	CAG	CGG	1488
Ile	Glu	Thr	Thr	Thr	Val	Pro	Gln	Asp	Ala	Val	Ser	Arg	Ser	Gln	Arg	
				485				490						495		
CGG	GGT	AGG	ACT	GGC	AGG	GGT	AGG	AGA	GGC	ATC	TAC	AGG	TTT	GTG	ACT	1536
Arg	Gly	Arg	Thr	Gly	Arg	Gly	Arg	Arg	Gly	Ile	Tyr	Arg	Phe	Val	Thr	
			500					505					510			
CCG	GGA	GAA	CGG	CCC	TCG	GGC	ATG	TTC	GAT	TCC	TCG	GTC	CTG	TGT	GAG	1584
Pro	Gly	Glu	Arg	Pro	Ser	Gly	Met	Phe	Asp	Ser	Ser	Val	Leu	Cys	Glu	
		515					520					525				
TGC	TAT	GAC	GCG	GGC	TGT	GCT	TGG	TAC	GAG	CTC	ACC	CCC	GCC	GAG	ACC	1632
Cys	Tyr	Asp	Ala	Gly	Cys	Ala	Trp	Tyr	Glu	Leu	Thr	Pro	Ala	Glu	Thr	
	530					535					540					
TCG	GTT	AGG	TTG	CGG	GCC	TAC	CTG	AAC	ACA	CCA	GGG	TTG	CCC	GTT	TGC	1680
Ser	Val	Arg	Leu	Arg	Ala	Tyr	Leu	Asn	Thr	Pro	Gly	Leu	Pro	Val	Cys	
545					550					555					560	
CAG	GAC	CAC	CTG	GAG	TTC	TGG	GAG	AGT	GTC	TTC	ACA	GGC	CTC	ACC	CAT	1728
Gln	Asp	His	Leu	Glu	Phe	Trp	Glu	Ser	Val	Phe	Thr	Gly	Leu	Thr	His	
			565					570						575		
ATA	GAT	GCA	CAC	TTC	TTG	TCC	CAG	ACC	AAG	CAG	GCA	GGA	GAC	AAC	TTC	1776
Ile	Asp	Ala	His	Phe	Leu	Ser	Gln	Thr	Lys	Gln	Ala	Gly	Asp	Asn	Phe	
			580					585					590			
CCC	TAC	CTG	GTA	GCA	TAC	CAA	GCC	ACG	GTG	TGC	GCC	AGG	GCT	CAG	GCC	1824
Pro	Tyr	Leu	Val	Ala	Tyr	Gln	Ala	Thr	Val	Cys	Ala	Arg	Ala	Gln	Ala	
		595					600					605				
CCA	CCT	CCA	TCA	TGG	GAT	CAA	ATG	TGG	AAG	TGT	CTC	ATA	CGG	CTG	AAA	1872
Pro	Pro	Pro	Ser	Trp	Asp	Gln	Met	Trp	Lys	Cys	Leu	Ile	Arg	Leu	Lys	
	610					615					620					
CCT	ACG	CTG	CAC	GGG	CCA	ACA	CCC	TTG	CTG	TAC	AGG	CTG	GGA	GCC	GTC	1920
Pro	Thr	Leu	His	Gly	Pro	Thr	Pro	Leu	Leu	Tyr	Arg	Leu	Gly	Ala	Val	

178

625	630	635	640	
CAA AAT GAG GTC ACC CTC ACC CAC CCC ATA ACC AAA TAC ATC ATG GCA				1968
Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala				
	645	650	655	
TGC ATG TCG GCT GAC CTG GAG GTC GTC ACT				1998
Cys Met Ser Ala Asp Leu Glu Val Val Thr				
	660	665		

## (2) INFORMATION FOR SEQ ID NO:105:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1998

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG	48
Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro	
1 5 10 15	
CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA	96
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	
20 25 30	
TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA	144
Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu	
35 40 45	
CTT GGT TGC AAG AAG ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC	192
Leu Gly Cys Lys Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val	
50 55 60	
GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG	240
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala	
65 70 75 80	
ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA	288
Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser	
85 90 95	
AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT	336
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn	
100 105 110	

GTG	GAC	CAG	GAC	CTC	GTC	GGC	TGG	CAG	GCG	CCC	CCC	GGG	GCG	CGT	TCC	384
Val	Asp	Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	
		115					120						125			
TTG	ACA	CCA	TGC	ACC	TGT	GGC	AGC	TCA	GAC	CTT	TAC	TTG	GTC	ACG	AGA	432
Leu	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	
	130					135					140					
CAT	GCT	GAC	GTC	ATT	CCG	GTG	CGC	CGG	CGG	GGC	GAC	AGT	AGG	GGG	AGC	480
His	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	
	145				150					155					160	
CTG	CTC	TCC	CCC	AGG	CCT	GTC	TCC	TAC	TTG	AAG	GGC	TCT	TCG	GGT	GGT	528
Leu	Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly	
				165					170					175		
CCA	CTG	CTC	TGC	CCT	TCG	GGG	CAC	GCT	GTG	GGC	ATC	TTC	CGG	GCT	GCC	576
Pro	Leu	Leu	Cys	Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	
			180					185					190			
GTA	TGC	ACC	CGG	GGG	GTT	GCG	AAG	GCG	GTG	GAC	TTT	GTG	CCC	GTA	GAG	624
Val	Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	
		195					200					205				
TCC	ATG	GAA	ACT	ACT	ATG	CGG	TCT	CCG	GTC	TTC	ACG	GAC	AAC	TCA	TCC	672
Ser	Met	Glu	Thr	Thr	Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser	Ser	
	210					215					220					
CCC	CCG	GCC	GTA	CCG	CAG	TCA	TTT	CAA	GTG	GCC	CAC	CTA	CAC	GCT	CCC	720
Pro	Pro	Ala	Val	Pro	Gln	Ser	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro	
	225				230					235					240	
ACT	GGC	AGC	GGC	AAG	AGT	ACT	AAA	GTG	CCG	GCT	GCA	TAT	GCA	GCC	CAA	768
Thr	Gly	Ser	Gly	Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	
				245				250						255		
GGG	TAC	AAG	GTG	CTC	GTC	CTC	AAT	CCG	TCC	GTT	GCC	GCT	ACC	TTA	GGG	816
Gly	Tyr	Lys	Val	Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly	
			260				265						270			
TTT	GGG	GCG	TAT	ATG	TCT	AAG	GCA	CAC	GGT	ATT	GAC	CCC	AAC	ATC	AGA	864
Phe	Gly	Ala	Tyr	Met	Ser	Lys	Ala	His	Gly	Ile	Asp	Pro	Asn	Ile	Arg	
		275					280					285				
ACT	GGG	GTA	AGG	ACC	ATT	ACC	ACA	GGC	GCC	CCC	GTC	ACA	TAC	TCT	ACC	912
Thr	Gly	Val	Arg	Thr	Ile	Thr	Thr	Gly	Ala	Pro	Val	Thr	Tyr	Ser	Thr	
		290				295					300					
TAT	GGC	AAG	TTT	CTT	GCC	GAT	GGT	GGT	TGC	TCT	GGG	GGC	GCT	TAT	GAC	960
Tyr	Gly	Lys	Phe	Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	
	305				310				315						320	
ATC	ATA	ATA	TGT	GAT	GAG	TGC	CAT	TCA	ACT	GAC	TCG	ACT	ACA	ATC	TTG	1008
Ile	Ile	Ile	Cys	Asp	Glu	Cys	His	Ser	Thr	Asp	Ser	Thr	Thr	Ile	Leu	
				325					330					335		
GGC	ATC	GGC	ACA	GTC	CTG	GAC	CAA	GCG	GAG	ACG	GCT	GGA	GCG	CGG	CTT	1056
Gly	Ile	Gly	Thr	Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	

340					345					350						
GTC	GTG	CTC	GCC	ACC	GCT	ACG	CCT	CCG	GGA	TCG	GTC	ACC	GTG	CCA	CAC	1104
Val	Val	Leu	Ala	Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Val	Pro	His	
		355					360					365				
CCA	AAC	ATC	GAG	GAG	GTG	GCC	CTG	TCT	AAT	ACT	GGA	GAG	ATC	CCC	TTC	1152
Pro	Asn	Ile	Glu	Glu	Val	Ala	Leu	Ser	Asn	Thr	Gly	Glu	Ile	Pro	Phe	
	370					375					380					
TAT	GGC	AAA	GCC	ATC	CCC	ATT	GAA	GCC	ATC	AGG	GGG	GGA	AGG	CAT	CTC	1200
Tyr	Gly	Lys	Ala	Ile	Pro	Ile	Glu	Ala	Ile	Arg	Gly	Gly	Arg	His	Leu	
385					390					395					400	
ATT	TTC	TGT	CAT	TCC	AAG	AAG	AAG	TGC	GAC	GAG	CTC	GCC	GCA	AAG	CTG	1248
Ile	Phe	Cys	His	Ser	Lys	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Ala	Lys	Leu	
				405					410					415		
TCA	GGC	CTC	GGA	ATC	AAC	GCT	GTG	GCG	TAT	TAC	CGG	GGG	CTC	GAT	GTG	1296
Ser	Gly	Leu	Gly	Ile	Asn	Ala	Val	Ala	Tyr	Tyr	Arg	Gly	Leu	Asp	Val	
			420				425						430			
TCC	GTC	ATA	CCA	ACT	ATC	GGA	GAC	GTC	GTT	GTC	GTG	GCA	ACA	GAC	GCT	1344
Ser	Val	Ile	Pro	Thr	Ile	Gly	Asp	Val	Val	Val	Val	GCA	Ala	Thr	Ala	
		435					440					445				
CTG	ATG	ACG	GGC	TAT	ACG	GGC	GAC	TTT	GAC	TCA	GTG	ATC	GAC	TGT	AAC	1392
Leu	Met	Thr	Gly	Tyr	Thr	Gly	Asp	Phe	Asp	Ser	Val	Ile	Asp	Cys	Asn	
	450					455					460					
ACA	TGT	GTC	ACC	CAG	ACA	GTC	GAC	TTC	AGC	TTG	GAT	CCC	ACC	TTC	ACC	1440
Thr	Cys	Val	Thr	Gln	Thr	Val	Asp	Phe	Ser	Leu	Asp	Pro	Thr	Phe	Thr	
465					470					475					480	
ATT	GAG	ACG	ACG	ACC	GTG	CCT	CAA	GAC	GCA	GTG	TCG	CGC	TCG	CAG	CGG	1488
Ile	Glu	Thr	Thr	Thr	Val	Pro	Gln	Asp	Ala	Val	Ser	Arg	Ser	Gln	Arg	
				485				490						495		
CGG	GGT	AGG	ACT	GGC	AGG	GGT	AGG	AGA	GGC	ATC	TAC	AGG	TTT	GTG	ACT	1536
Arg	Gly	Arg	Thr	Gly	Arg	Gly	Arg	Arg	Gly	Ile	Tyr	Arg	Phe	Val	Thr	
			500					505					510			
CCG	GGA	GAA	CGG	CCC	TCG	GGC	ATG	TTC	GAT	TCC	TCG	GTC	CTG	TGT	GAG	1584
Pro	Gly	Glu	Arg	Pro	Ser	Gly	Met	Phe	Asp	Ser	Ser	Val	Leu	Cys	Glu	
		515					520					525				
TGC	TAT	GAC	GCG	GGC	TGT	GCT	TGG	TAC	GAG	CTC	ACC	CCC	GCC	GAG	ACC	1632
Cys	Tyr	Asp	Ala	Gly	Cys	Ala	Trp	Tyr	Glu	Leu	Thr	Pro	Ala	Glu	Thr	
	530					535					540					
TCG	GTT	AGG	TTG	CGG	GCC	TAC	CTG	AAC	ACA	CCA	GGG	TTG	CCC	GTT	TGC	1680
Ser	Val	Arg	Leu	Arg	Ala	Tyr	Leu	Asn	Thr	Pro	Gly	Leu	Pro	Val	Cys	
545					550					555					560	
CAG	GAC	CAC	CTG	GAG	TTC	TGG	GAG	AGT	GTC	TTC	ACA	GGC	CTC	ACC	CAT	1728
Gln	Asp	His	Leu	Glu	Phe	Trp	Glu	Ser	Val	Phe	Thr	Gly	Leu	Thr	His	
				565					570					575		



ATA GAT GCA CAC TTC TTG TCC CAG ACC AAG CAG GCA GGA GAC AAC TTC	1776
Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe	
580 585 590	
CCC TAC CTG GTA GCA TAC CAA GCC ACG GTG TGC GCC AGG GCT CAG GCC	1824
Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala	
595 600 605	
CCA CCT CCA TCA TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA	1872
Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys	
610 615 620	
CCT ACG CTG CAC GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC	1920
Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val	
625 630 635 640	
CAA AAT GAG GTC ACC CTC ACC CAC CCC ATA ACC AAA TAC ATC ATG GCA	1968
Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala	
645 650 655	
TGC ATG TCG GCT GAC CTG GAG GTC GTC ACT	1998
Cys Met Ser Ala Asp Leu Glu Val Val Thr	
660 665	

## (2) INFORMATION FOR SEQ ID NO:106:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1998

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG	48
Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro	
1 5 10 15	
CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA	96
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	
20 25 30	
TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA	144
Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu	
35 40 45	
CTT GGT TGC ATC ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC	192
Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val	
50 55 60	

GAG	GGA	GAG	GTT	CAG	GTG	GTT	TCC	ACC	GCA	ACA	CAA	TCC	TTC	CTG	GCG	240
Glu	Gly	Glu	Val	Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala	
65					70					75					80	
ACC	TGC	GTC	AAC	GGC	GTG	TGT	TGG	ACC	GTT	TAC	CAT	GGT	GCT	GGC	TCA	288
Thr	Cys	Val	Asn	Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser	
				85					90					95		
AAG	ACC	TTA	GCC	GGC	CCA	AAG	GGG	CCA	ATC	ACC	CAG	ATG	TAC	ACT	AAT	336
Lys	Thr	Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	
			100					105					110			
GTG	GAC	CAG	GAC	CTC	GTC	GGC	TGG	CAG	GCG	CCC	CCC	GGG	GCG	CGT	TCC	384
Val	Asp	Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	
		115					120					125				
TTG	ACA	CCA	TGC	ACC	TGT	GGC	AGC	TCA	GAC	CTT	TAC	TTG	GTC	ACG	AGA	432
Leu	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	
	130					135					140					
CAT	GCT	GAC	GTC	ATT	CCG	GTG	CGC	CGG	CGG	GGC	GAC	AGT	AGG	GGG	AGC	480
His	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	
145					150					155					160	
CTG	CTC	TCC	CCC	AGG	CCT	GTC	TCC	TAC	TTG	AAG	GGC	TCT	GCT	GGT	GGT	528
Leu	Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ala	Gly	Gly	
				165					170					175		
CCA	CTG	CTC	TGC	CCT	TCG	GGG	CAC	GCT	GTG	GGC	ATC	TTC	CGG	GCT	GCC	576
Pro	Leu	Leu	Cys	Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	
			180					185					190			
GTA	TGC	ACC	CGG	GGG	GTT	GCG	AAG	GCG	GTG	GAC	TTT	GTG	CCC	GTA	GAG	624
Val	Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	
		195					200					205				
TCC	ATG	GAA	ACT	ACT	ATG	CGG	TCT	CCG	GTC	TTC	ACG	GAC	AAC	TCA	TCC	672
Ser	Met	Glu	Thr	Thr	Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser	Ser	
	210					215					220					
CCC	CCG	GCC	GTA	CCG	CAG	TCA	TTT	CAA	GTG	GCC	CAC	CTA	CAC	GCT	CCC	720
Pro	Pro	Ala	Val	Pro	Gln	Ser	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro	
225					230					235					240	
ACT	GGC	AGC	GGC	AAG	AGT	ACT	AAA	GTG	CCG	GCT	GCA	TAT	GCA	GCC	CAA	768
Thr	Gly	Ser	Gly	Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	
				245				250						255		
GGG	TAC	AAG	GTG	CTC	GTC	CTC	AAT	CCG	TCC	GTT	GCC	GCT	ACC	TTA	GGG	816
Gly	Tyr	Lys	Val	Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly	
			260					265					270			
TTT	GGG	GCG	TAT	ATG	TCT	AAG	GCA	CAC	GGT	ATT	GAC	CCC	AAC	ATC	AGA	864
Phe	Gly	Ala	Tyr	Met	Ser	Lys	Ala	His	Gly	Ile	Asp	Pro	Asn	Ile	Arg	
		275					280					285				
ACT	GGG	GTA	AGG	ACC	ATT	ACC	ACA	GGC	GCC	CCC	GTC	ACA	TAC	TCT	ACC	912

Thr	Gly	Val	Arg	Thr	Ile	Thr	Thr	Gly	Ala	Pro	Val	Thr	Tyr	Ser	Thr	
290						295					300					
TAT	GGC	AAG	TTT	CTT	GCC	GAT	GGT	GGT	TGC	TCT	GGG	GGC	GCT	TAT	GAC	960
Tyr	Gly	Lys	Phe	Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	
305					310					315					320	
ATC	ATA	ATA	TGT	GAT	GAG	TGC	CAT	TCA	ACT	GAC	TCG	ACT	ACA	ATC	TTG	1008
Ile	Ile	Ile	Cys	Asp	Glu	Cys	His	Ser	Thr	Asp	Ser	Thr	Thr	Ile	Leu	
				325					330						335	
GGC	ATC	GGC	ACA	GTC	CTG	GAC	CAA	GCG	GAG	ACG	GCT	GGA	GCG	CGG	CTT	1056
Gly	Ile	Gly	Thr	Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	
				340				345							350	
GTC	GTG	CTC	GCC	ACC	GCT	ACG	CCT	CCG	GGA	TCG	GTC	ACC	GTG	CCA	CAC	1104
Val	Val	Leu	Ala	Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Val	Pro	His	
				355				360							365	
CCA	AAC	ATC	GAG	GAG	GTG	GCC	CTG	TCT	AAT	ACT	GGA	GAG	ATC	CCC	TTC	1152
Pro	Asn	Ile	Glu	Glu	Val	Ala	Leu	Ser	Asn	Thr	Gly	Glu	Ile	Pro	Phe	
	370						375								380	
TAT	GGC	AAA	GCC	ATC	CCC	ATT	GAA	GCC	ATC	AGG	GGG	GGA	AGG	CAT	CTC	1200
Tyr	Gly	Lys	Ala	Ile	Pro	Ile	Glu	Ala	Ile	Arg	Gly	Gly	Arg	His	Leu	
385					390					395					400	
ATT	TTC	TGT	CAT	TCC	AAG	AAG	AAG	TGC	GAC	GAG	CTC	GCC	GCA	AAG	CTG	1248
Ile	Phe	Cys	His	Ser	Lys	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Ala	Lys	Leu	
				405					410						415	
TCA	GGC	CTC	GGA	ATC	AAC	GCT	GTG	GCG	TAT	TAC	CGG	GGG	CTC	GAT	GTG	1296
Ser	Gly	Leu	Gly	Ile	Asn	Ala	Val	Ala	Tyr	Tyr	Arg	Gly	Leu	Asp	Val	
				420				425							430	
TCC	GTC	ATA	CCA	ACT	ATC	GGA	GAC	GTC	GTT	GTC	GTG	GCA	ACA	GAC	GCT	1344
Ser	Val	Ile	Pro	Thr	Ile	Gly	Asp	Val	Val	Val	Val	Ala	Thr	Asp	Ala	
				435				440							445	
CTG	ATG	ACG	GGC	TAT	ACG	GGC	GAC	TTT	GAC	TCA	GTG	ATC	GAC	TGT	AAC	1392
Leu	Met	Thr	Gly	Tyr	Thr	Gly	Asp	Phe	Asp	Ser	Val	Ile	Asp	Cys	Asn	
	450						455								460	
ACA	TGT	GTC	ACC	CAG	ACA	GTC	GAC	TTC	AGC	TTG	GAT	CCC	ACC	TTC	ACC	1440
Thr	Cys	Val	Thr	Gln	Thr	Val	Asp	Phe	Ser	Leu	Asp	Pro	Thr	Phe	Thr	
	465					470					475				480	
ATT	GAG	ACG	ACG	ACC	GTG	CCT	CAA	GAC	GCA	GTG	TCG	CGC	TCG	CAG	CGG	1488
Ile	Glu	Thr	Thr	Thr	Val	Pro	Gln	Asp	Ala	Val	Ser	Arg	Ser	Gln	Arg	
				485					490						495	
CGG	GGT	AGG	ACT	GGC	AGG	GGT	AGG	AGA	GGC	ATC	TAC	AGG	TTT	GTG	ACT	1536
Arg	Gly	Arg	Thr	Gly	Arg	Gly	Arg	Arg	Gly	Ile	Tyr	Arg	Phe	Val	Thr	
				500				505							510	
CCG	GGA	GAA	CGG	CCC	TCG	GGC	ATG	TTC	GAT	TCC	TCG	GTC	CTG	TGT	GAG	1584
Pro	Gly	Glu	Arg	Pro	Ser	Gly	Met	Phe	Asp	Ser	Ser	Val	Leu	Cys	Glu	
				515			520								525	

TGC TAT GAC GCG GGC TGT GCT TGG TAC GAG CTC ACC CCC GCC GAG ACC	1632
Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr	
530 535 540	
TCG GTT AGG TTG CGG GCC TAC CTG AAC ACA CCA GGG TTG CCC GTT TGC	1680
Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys	
545 550 555 560	
CAG GAC CAC CTG GAG TTC TGG GAG AGT GTC TTC ACA GGC CTC ACC CAT	1728
Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His	
565 570 575	
ATA GAT GCA CAC TTC TTG TCC CAG ACC AAG CAG GCA GGA GAC AAC TTC	1776
Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe	
580 585 590	
CCC TAC CTG GTA GCA TAC CAA GCC ACG GTG TGC GCC AGG GCT CAG GCC	1824
Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala	
595 600 605	
CCA CCT CCA TCA TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA	1872
Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys	
610 615 620	
CCT ACG CTG CAC GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC	1920
Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val	
625 630 635 640	
CAA AAT GAG GTC ACC CTC ACC CAC CCC ATA ACC AAA TAC ATC ATG GCA	1968
Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala	
645 650 655	
TGC ATG TCG GCT GAC CTG GAG GTC GTC ACT	1998
Cys Met Ser Ala Asp Leu Glu Val Val Thr	
660 665	

## (2) INFORMATION FOR SEQ ID NO:107:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1998

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG	48
Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro	

155

1	5	10	15	
CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA				96
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	20	25	30	
TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA				144
Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu	35	40	45	
CTT GGT TGC AAG ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC				192
Leu Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val	50	55	60	
GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG				240
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala	65	70	75	80
ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA				288
Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser	85	90	95	
AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT				336
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn	100	105	110	
GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC				384
Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser	115	120	125	
TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA				432
Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg	130	135	140	
CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC				480
His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser	145	150	155	160
CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT GCT GGT GGT				528
Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly	165	170	175	
CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC				576
Pro Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala	180	185	190	
GTA TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG				624
Val Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu	195	200	205	
TCC ATG GAA ACT ACT ATG CGG TCT CCG GTC TTC ACG GAC AAC TCA TCC				672
Ser Met Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser	210	215	220	
CCC CCG GCC GTA CCG CAG TCA TTT CAA GTG GCC CAC CTA CAC GCT CCC				720
Pro Pro Ala Val Pro Gln Ser Phe Gln Val Ala His Leu His Ala Pro	225	230	235	240

ACT	GGC	AGC	GGC	AAG	AGT	ACT	AAA	GTG	CCG	GCT	GCA	TAT	GCA	GCC	CAA	768
Thr	Gly	Ser	Gly	Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	
				245					250						255	
GGG	TAC	AAG	GTG	CTC	GTC	CTC	AAT	CCG	TCC	GTT	GCC	GCT	ACC	TTA	GGG	816
Gly	Tyr	Lys	Val	Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly	
			260					265					270			
TTT	GGG	GCG	TAT	ATG	TCT	AAG	GCA	CAC	GGT	ATT	GAC	CCC	AAC	ATC	AGA	864
Phe	Gly	Ala	Tyr	Met	Ser	Lys	Ala	His	Gly	Ile	Asp	Pro	Asn	Ile	Arg	
		275					280					285				
ACT	GGG	GTA	AGG	ACC	ATT	ACC	ACA	GGC	GCC	CCC	GTC	ACA	TAC	TCT	ACC	912
Thr	Gly	Val	Arg	Thr	Ile	Thr	Thr	Gly	Ala	Pro	Val	Thr	Tyr	Ser	Thr	
	290					295					300					
TAT	GGC	AAG	TTT	CTT	GCC	GAT	GGT	GGT	TGC	TCT	GGG	GGC	GCT	TAT	GAC	960
Tyr	Gly	Lys	Phe	Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	
305					310				315						320	
ATC	ATA	ATA	TGT	GAT	GAG	TGC	CAT	TCA	ACT	GAC	TCG	ACT	ACA	ATC	TTG	1008
Ile	Ile	Ile	Cys	Asp	Glu	Cys	His	Ser	Thr	Asp	Ser	Thr	Thr	Ile	Leu	
			325					330						335		
GGC	ATC	GGC	ACA	GTC	CTG	GAC	CAA	GCG	GAG	ACG	GCT	GGA	GCG	CGG	CTT	1056
Gly	Ile	Gly	Thr	Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	
			340					345					350			
GTC	GTG	CTC	GCC	ACC	GCT	ACG	CCT	CCG	GGA	TCG	GTC	ACC	GTG	CCA	CAC	1104
Val	Val	Leu	Ala	Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Val	Pro	His	
		355					360					365				
CCA	AAC	ATC	GAG	GAG	GTG	GCC	CTG	TCT	AAT	ACT	GGA	GAG	ATC	CCC	TTC	1152
Pro	Asn	Ile	Glu	Glu	Val	Ala	Leu	Ser	Asn	Thr	Gly	Glu	Ile	Pro	Phe	
	370					375					380					
TAT	GGC	AAA	GCC	ATC	CCC	ATT	GAA	GCC	ATC	AGG	GGG	GGA	AGG	CAT	CTC	1200
Tyr	Gly	Lys	Ala	Ile	Pro	Ile	Glu	Ala	Ile	Arg	Gly	Gly	Arg	His	Leu	
385					390					395					400	
ATT	TTC	TGT	CAT	TCC	AAG	AAG	AAG	TGC	GAC	GAG	CTC	GCC	GCA	AAG	CTG	1248
Ile	Phe	Cys	His	Ser	Lys	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Ala	Lys	Leu	
				405					410					415		
TCA	GGC	CTC	GGA	ATC	AAC	GCT	GTG	GCG	TAT	TAC	CGG	GGG	CTC	GAT	GTG	1296
Ser	Gly	Leu	Gly	Ile	Asn	Ala	Val	Ala	Tyr	Tyr	Arg	Gly	Leu	Asp	Val	
			420				425						430			
TCC	GTC	ATA	CCA	ACT	ATC	GGA	GAC	GTC	GTT	GTC	GTG	GCA	ACA	GAC	GCT	1344
Ser	Val	Ile	Pro	Thr	Ile	Gly	Asp	Val	Val	Val	Val	Ala	Thr	Asp	Ala	
		435				440						445				
CTG	ATG	ACG	GGC	TAT	ACG	GGC	GAC	TTT	GAC	TCA	GTG	ATC	GAC	TGT	AAC	1392
Leu	Met	Thr	Gly	Tyr	Thr	Gly	Asp	Phe	Asp	Ser	Val	Ile	Asp	Cys	Asn	
	450					455					460					
ACA	TGT	GTC	ACC	CAG	ACA	GTC	GAC	TTC	AGC	TTG	GAT	CCC	ACC	TTC	ACC	1440
Thr	Cys	Val	Thr	Gln	Thr	Val	Asp	Phe	Ser	Leu	Asp	Pro	Thr	Phe	Thr	

465		470		475		480	
ATT GAG ACG ACG ACC GTG CCT CAA GAC GCA GTG TCG CGC TCG CAG CGG	1488						
Ile Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg							
		485		490		495	
CGG GGT AGG ACT GGC AGG GGT AGG AGA GGC ATC TAC AGG TTT GTG ACT	1536						
Arg Gly Arg Thr Thr Gly Arg Gly Arg Arg Gly Ile Tyr Arg Phe Val Thr		500		505		510	
CCG GGA GAA CGG CCC TCG GGC ATG TTC GAT TCC TCG GTC CTG TGT GAG	1584						
Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu		515		520		525	
TGC TAT GAC GCG GGC TGT GCT TGG TAC GAG CTC ACC CCC GCC GAG ACC	1632						
Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr		530		535		540	
TCG GTT AGG TTG CGG GCC TAC CTG AAC ACA CCA GGG TTG CCC GTT TGC	1680						
Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys		545		550		555	560
CAG GAC CAC CTG GAG TTC TGG GAG AGT GTC TTC ACA GGC CTC ACC CAT	1728						
Gln Asp His Leu Phe Thr Glu Ser Val Phe Thr Gly Leu Thr His		565		570		575	
ATA GAT GCA CAC TTC TTG TCC CAG ACC AAG CAG GCA GGA GAC AAC TTC	1776						
Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe		580		585		590	
CCC TAC CTG GTA GCA TAC CAA GCC ACG GTG TGC GCC AGG GCT CAG GCC	1824						
Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala		595		600		605	
CCA CCT CCA TCA TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA	1872						
Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys		610		615		620	
CCT ACG CTG CAC GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC	1920						
Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val		625		630		635	640
CAA AAT GAG GTC ACC CTC ACC CAC CCC ATA ACC AAA TAC ATC ATG GCA	1968						
Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala		645		650		655	
TGC ATG TCG GCT GAC CTG GAG GTC GTC ACT	1998						
Cys Met Ser Ala Asp Leu Glu Val Val Thr		660		665			

## (2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1998 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

158

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1998

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108

ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG	48
Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro	
1 5 10 15	
CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA	96
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	
20 25 30	
TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA	144
Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu	
35 40 45	
CTT GGT TGC ATC AAG ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC	192
Leu Gly Cys Ile Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val	
50 55 60	
GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG	240
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala	
65 70 75 80	
ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA	288
Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser	
85 90 95	
AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT	336
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn	
100 105 110	
GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC	384
Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser	
115 120 125	
TTG ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA	432
Leu Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg	
130 135 140	
CAT GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC	480
His Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser	
145 150 155 160	
CTG CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT GCT GGT GGT	528
Leu Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ala Gly Gly	
165 170 175	
CCA CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC	576



Pro	Leu	Leu	Cys	Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	
			180					185					190			
GTA	TGC	ACC	CGG	GGG	GTT	GCG	AAG	GCG	GTG	GAC	TTT	GTG	CCC	GTA	GAG	624
Val	Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	
		195					200					205				
TCC	ATG	GAA	ACT	ACT	ATG	CGG	TCT	CCG	GTC	TTC	ACG	GAC	AAC	TCA	TCC	672
Ser	Met	Glu	Thr	Thr	Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser	Ser	
	210					215					220					
CCC	CCG	GCC	GTA	CCG	CAG	TCA	TTT	CAA	GTG	GCC	CAC	CTA	CAC	GCT	CCC	720
Pro	Pro	Ala	Val	Pro	Gln	Ser	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro	
225					230					235					240	
ACT	GGC	AGC	GGC	AAG	AGT	ACT	AAA	GTG	CCG	GCT	GCA	TAT	GCA	GCC	CAA	768
Thr	Gly	Ser	Gly	Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	
				245				250						255		
GGG	TAC	AAG	GTG	CTC	GTC	CTC	AAT	CCG	TCC	GTT	GCC	GCT	ACC	TTA	GGG	816
Gly	Tyr	Lys	Val	Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly	
			260				265						270			
TTT	GGG	GCG	TAT	ATG	TCT	AAG	GCA	CAC	GGT	ATT	GAC	CCC	AAC	ATC	AGA	864
Phe	Gly	Ala	Tyr	Met	Ser	Lys	Ala	His	Gly	Ile	Asp	Pro	Asn	Ile	Arg	
		275				280						285				
ACT	GGG	GTA	AGG	ACC	ATT	ACC	ACA	GGC	GCC	CCC	GTC	ACA	TAC	TCT	ACC	912
Thr	Gly	Val	Arg	Thr	Ile	Thr	Thr	Gly	Ala	Pro	Val	Thr	Tyr	Ser	Thr	
	290					295					300					
TAT	GGC	AAG	TTT	CTT	GCC	GAT	GGT	GGT	TGC	TCT	GGG	GGC	GCT	TAT	GAC	960
Tyr	Gly	Lys	Phe	Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	
305					310				315						320	
ATC	ATA	ATA	TGT	GAT	GAG	TGC	CAT	TCA	ACT	GAC	TCG	ACT	ACA	ATC	TTG	1008
Ile	Ile	Ile	Cys	Asp	Glu	Cys	His	Ser	Thr	Asp	Ser	Thr	Thr	Ile	Leu	
			325						330					335		
GGC	ATC	GGC	ACA	GTC	CTG	GAC	CAA	GCG	GAG	ACG	GCT	GGA	GCG	CGG	CTT	1056
Gly	Ile	Gly	Thr	Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	
			340				345						350			
GTC	GTG	CTC	GCC	ACC	GCT	ACG	CCT	CCG	GGA	TCG	GTC	ACC	GTG	CCA	CAC	1104
Val	Val	Leu	Ala	Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Val	Pro	His	
		355					360					365				
CCA	AAC	ATC	GAG	GAG	GTG	GCC	CTG	TCT	AAT	ACT	GGA	GAG	ATC	CCC	TTC	1152
Pro	Asn	Ile	Glu	Glu	Val	Ala	Leu	Ser	Asn	Thr	Gly	Glu	Ile	Pro	Phe	
	370					375					380					
TAT	GGC	AAA	GCC	ATC	CCC	ATT	GAA	GCC	ATC	AGG	GGG	GGA	AGG	CAT	CTC	1200
Tyr	Gly	Lys	Ala	Ile	Pro	Ile	Glu	Ala	Ile	Arg	Gly	Gly	Arg	His	Leu	
385					390					395					400	
ATT	TTC	TGT	CAT	TCC	AAG	AAG	AAG	TGC	GAC	GAG	CTC	GCC	GCA	AAG	CTG	1248
Ile	Phe	Cys	His	Ser	Lys	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Ala	Lys	Leu	
				405					410						415	

TCA	GGC	CTC	GGA	ATC	AAC	GCT	GTG	GCG	TAT	TAC	CGG	GGG	CTC	GAT	GTG	1296
Ser	Gly	Leu	Gly	Ile	Asn	Ala	Val	Ala	Tyr	Tyr	Arg	Gly	Leu	Asp	Val	
			420					425					430			
TCC	GTC	ATA	CCA	ACT	ATC	GGA	GAC	GTC	GTT	GTC	GTG	GCA	ACA	GAC	GCT	1344
Ser	Val	Ile	Pro	Thr	Ile	Gly	Asp	Val	Val	Val	Val	Ala	Thr	Asp	Ala	
			435					440					445			
CTG	ATG	ACG	GGC	TAT	ACG	GGC	GAC	TTT	GAC	TCA	GTG	ATC	GAC	TGT	AAC	1392
Leu	Met	Thr	Gly	Tyr	Thr	Gly	Asp	Phe	Asp	Ser	Val	Ile	Asp	Cys	Asn	
	450					455					460					
ACA	TGT	GTC	ACC	CAG	ACA	GTC	GAC	TTC	AGC	TTG	GAT	CCC	ACC	TTC	ACC	1440
Thr	Cys	Val	Thr	Gln	Thr	Val	Asp	Phe	Ser	Leu	Asp	Pro	Thr	Phe	Thr	
465						470				475					480	
ATT	GAG	ACG	ACG	ACC	GTG	CCT	CAA	GAC	GCA	GTG	TCG	CGC	TCG	CAG	CGG	1488
Ile	Glu	Thr	Thr	Thr	Val	Pro	Gln	Asp	Ala	Val	Ser	Arg	Ser	Gln	Arg	
				485					490					495		
CGG	GGT	AGG	ACT	GGC	AGG	GGT	AGG	AGA	GGC	ATC	TAC	AGG	TTT	GTG	ACT	1536
Arg	Gly	Arg	Thr	Gly	Arg	Gly	Arg	Arg	Gly	Ile	Tyr	Arg	Phe	Val	Thr	
			500					505					510			
CCG	GGA	GAA	CGG	CCC	TCG	GGC	ATG	TTC	GAT	TCC	TCG	GTC	CTG	TGT	GAG	1584
Pro	Gly	Glu	Arg	Pro	Ser	Gly	Met	Phe	Asp	Ser	Ser	Val	Leu	Cys	Glu	
		515					520					525				
TGC	TAT	GAC	GCG	GGC	TGT	GCT	TGG	TAC	GAG	CTC	ACC	CCC	GCC	GAG	ACC	1632
Cys	Tyr	Asp	Ala	Gly	Cys	Ala	Trp	Tyr	Glu	Leu	Thr	Pro	Ala	Glu	Thr	
	530					535					540					
TCG	GTT	AGG	TTG	CGG	GCC	TAC	CTG	AAC	ACA	CCA	GGG	TTG	CCC	GTT	TGC	1680
Ser	Val	Arg	Leu	Arg	Ala	Tyr	Leu	Asn	Thr	Pro	Gly	Leu	Pro	Val	Cys	
545					550					555					560	
CAG	GAC	CAC	CTG	GAG	TTC	TGG	GAG	AGT	GTC	TTC	ACA	GGC	CTC	ACC	CAT	1728
Gln	Asp	His	Leu	Glu	Phe	Trp	Glu	Ser	Val	Phe	Thr	Gly	Leu	Thr	His	
				565					570					575		
ATA	GAT	GCA	CAC	TTC	TTG	TCC	CAG	ACC	AAG	CAG	GCA	GGA	GAC	AAC	TTC	1776
Ile	Asp	Ala	His	Phe	Leu	Ser	Gln	Thr	Lys	Gln	Ala	Gly	Asp	Asn	Phe	
			580					585					590			
CCC	TAC	CTG	GTA	GCA	TAC	CAA	GCC	ACG	GTG	TGC	GCC	AGG	GCT	CAG	GCC	1824
Pro	Tyr	Leu	Val	Ala	Tyr	Gln	Ala	Thr	Val	Cys	Ala	Arg	Ala	Gln	Ala	
		595					600					605				
CCA	CCT	CCA	TCA	TGG	GAT	CAA	ATG	TGG	AAG	TGT	CTC	ATA	CGG	CTG	AAA	1872
Pro	Pro	Pro	Ser	Trp	Asp	Gln	Met	Trp	Lys	Cys	Leu	Ile	Arg	Leu	Lys	
		610				615					620					
CCT	ACG	CTG	CAC	GGG	CCA	ACA	CCC	TTG	CTG	TAC	AGG	CTG	GGA	GCC	GTC	1920
Pro	Thr	Leu	His	Gly	Pro	Thr	Pro	Leu	Leu	Tyr	Arg	Leu	Gly	Ala	Val	
625					630					635					640	
CAA	AAT	GAG	GTC	ACC	CTC	ACC	CAC	CCC	ATA	ACC	AAA	TAC	ATC	ATG	GCA	1968

Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala  
                                 645                                650                                655

TGC ATG TCG GCT GAC CTG GAG GTC GTC ACT  
 Cys Met Ser Ala Asp Leu Glu Val Val Thr  
                                 660                                665

1998

## (2) INFORMATION FOR SEQ ID NO:109:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1998

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG	48
Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro	
1                                5                                10                                15	
CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA	96
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	
20                                25                                30	
TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA	144
Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu	
35                                40                                45	
CTT GGT TGC AAG AAG ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC	192
Leu Gly Cys Lys Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val	
50                                55                                60	
GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG	240
Glu Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala	
65                                70                                75                                80	
ACC TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA	288
Thr Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser	
85                                90                                95	
AAG ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT	336
Lys Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn	
100                                105                                110	
GTG GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC	384
Val Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser	
115                                120                                125	

TTG	ACA	CCA	TGC	ACC	TGT	GGC	AGC	TCA	GAC	CTT	TAC	TTG	GTC	ACG	AGA	432
Leu	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	
	130					135					140					
CAT	GCT	GAC	GTC	ATT	CCG	GTG	CGC	CGG	CGG	GGC	GAC	AGT	AGG	GGG	AGC	480
His	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	
145					150					155					160	
CTG	CTC	TCC	CCC	AGG	CCT	GTC	TCC	TAC	TTG	AAG	GGC	TCT	GCT	GGT	GGT	528
Leu	Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ala	Gly	Gly	
				165					170					175		
CCA	CTG	CTC	TGC	CCT	TCG	GGG	CAC	GCT	GTG	GGC	ATC	TTC	CGG	GCT	GCC	576
Pro	Leu	Leu	Cys	Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	
			180					185					190			
GTA	TGC	ACC	CGG	GGG	GTT	GCG	AAG	GCG	GTG	GAC	TTT	GTG	CCC	GTA	GAG	624
Val	Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	
	195						200					205				
TCC	ATG	GAA	ACT	ACT	ATG	CGG	TCT	CCG	GTC	TTC	ACG	GAC	AAC	TCA	TCC	672
Ser	Met	Glu	Thr	Thr	Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser	Ser	
	210					215					220					
CCC	CCG	GCC	GTA	CCG	CAG	TCA	TTT	CAA	GTG	GCC	CAC	CTA	CAC	GCT	CCC	720
Pro	Pro	Ala	Val	Pro	Gln	Ser	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro	
225					230					235					240	
ACT	GGC	AGC	GGC	AAG	AGT	ACT	AAA	GTG	CCG	GCT	GCA	TAT	GCA	GCC	CAA	768
Thr	Gly	Ser	Gly	Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	
				245					250					255		
GGG	TAC	AAG	GTG	CTC	GTC	CTC	AAT	CCG	TCC	GTT	GCC	GCT	ACC	TTA	GGG	816
Gly	Tyr	Lys	Val	Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly	
			260					265					270			
TTT	GGG	GCG	TAT	ATG	TCT	AAG	GCA	CAC	GGT	ATT	GAC	CCC	AAC	ATC	AGA	864
Phe	Gly	Ala	Tyr	Met	Ser	Lys	Ala	His	Gly	Ile	Asp	Pro	Asn	Ile	Arg	
	275						280					285				
ACT	GGG	GTA	AGG	ACC	ATT	ACC	ACA	GGC	GCC	CCC	GTC	ACA	TAC	TCT	ACC	912
Thr	Gly	Val	Arg	Thr	Ile	Thr	Thr	Gly	Ala	Pro	Val	Thr	Tyr	Ser	Thr	
	290					295					300					
TAT	GGC	AAG	TTT	CTT	GCC	GAT	GGT	GGT	TGC	TCT	GGG	GGC	GCT	TAT	GAC	960
Tyr	Gly	Lys	Phe	Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	
305					310					315					320	
ATC	ATA	ATA	TGT	GAT	GAG	TGC	CAT	TCA	ACT	GAC	TCG	ACT	ACA	ATC	TTG	1008
Ile	Ile	Ile	Cys	Asp	Glu	Cys	His	Ser	Thr	Asp	Ser	Thr	Thr	Ile	Leu	
				325					330					335		
GGC	ATC	GGC	ACA	GTC	CTG	GAC	CAA	GCG	GAG	ACG	GCT	GGA	GCG	CGG	CTT	1056
Gly	Ile	Gly	Thr	Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	
			340					345					350			
GTC	GTG	CTC	GCC	ACC	GCT	ACG	CCT	CCG	GGA	TCG	GTC	ACC	GTG	CCA	CAC	1104
Val	Val	Leu	Ala	Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Val	Pro	His	

355	360	365	
CCA AAC ATC GAG GAG GTG GCC CTG TCT AAT ACT GGA GAG ATC CCC TTC Pro Asn Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe 370 375 380			1152
TAT GGC AAA GCC ATC CCC ATT GAA GCC ATC AGG GGG GGA AGG CAT CTC Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu 385 390 395 400			1200
ATT TTC TGT CAT TCC AAG AAG AAG TGC GAC GAG CTC GCC GCA AAG CTG Ile Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu 405 410 415			1248
TCA GGC CTC GGA ATC AAC GCT GTG GCG TAT TAC CGG GGG CTC GAT GTG Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val 420 425 430			1296
TCC GTC ATA CCA ACT ATC GGA GAC GTC GTT GTC GTG GCA ACA GAC GCT Ser Val Ile Pro Thr Ile Gly Asp Val Val Val Val Ala Thr Asp Ala 435 440 445			1344
CTG ATG ACG GGC TAT ACG GGC GAC TTT GAC TCA GTG ATC GAC TGT AAC Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn 450 455 460			1392
ACA TGT GTC ACC CAG ACA GTC GAC TTC AGC TTG GAT CCC ACC TTC ACC Thr Cys Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr 465 470 475 480			1440
ATT GAG ACG ACG ACC GTG CCT CAA GAC GCA GTG TCG CGC TCG CAG CGG Ile Glu Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg 485 490 495			1488
CGG GGT AGG ACT GGC AGG GGT AGG AGA GGC ATC TAC AGG TTT GTG ACT Arg Gly Arg Thr Gly Arg Gly Arg Arg Gly Ile Tyr Arg Phe Val Thr 500 505 510			1536
CCG GGA GAA CGG CCC TCG GGC ATG TTC GAT TCC TCG GTC CTG TGT GAG Pro Gly Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu 515 520 525			1584
TGC TAT GAC GCG GGC TGT GCT TGG TAC GAG CTC ACC CCC GCC GAG ACC Cys Tyr Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr 530 535 540			1632
TCG GTT AGG TTG CGG GCC TAC CTG AAC ACA CCA GGG TTG CCC GTT TGC Ser Val Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys 545 550 555 560			1680
CAG GAC CAC CTG GAG TTC TGG GAG AGT GTC TTC ACA GGC CTC ACC CAT Gln Asp His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His 565 570 575			1728
ATA GAT GCA CAC TTC TTG TCC CAG ACC AAG CAG GCA GGA GAC AAC TTC Ile Asp Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe 580 585 590			1776

CCC TAC CTG GTA GCA TAC CAA GCC ACG GTG TGC GCC AGG GCT CAG GCC	1824
Pro Tyr Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala	
595 600 605	
CCA CCT CCA TCA TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA	1872
Pro Pro Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys	
610 615 620	
CCT ACG CTG CAC GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC	1920
Pro Thr Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val	
625 630 635 640	
CAA AAT GAG GTC ACC CTC ACC CAC CCC ATA ACC AAA TAC ATC ATG GCA	1968
Gln Asn Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala	
645 650 655	
TGC ATG TCG GCT GAC CTG GAG GTC GTC ACT	1998
Cys Met Ser Ala Asp Leu Glu Val Val Thr	
660 665	

## (2) INFORMATION FOR SEQ ID NO:110:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2016 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2016

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG	48
Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro	
1 5 10 15	
CGC GGC AGC CAT ATG GCT TAC TCT CTG ACT ACG GGT TCT GTT GTT ATT	96
Arg Gly Ser His Met Ala Tyr Ser Leu Thr Thr Gly Ser Val Val Ile	
20 25 30	
GTT GGT AGA ATT ATT TTA TCT GGT AGT GGT AGT ATC ACG GCC TAC TCC	144
Val Gly Arg Ile Ile Leu Ser Gly Ser Gly Ser Ile Thr Ala Tyr Ser	
35 40 45	
CAA CAG ACG CGG GGC CTA CTT GGT TGC ATC ATC ACT AGC CTT ACA GGC	192
Gln Gln Thr Arg Gly Leu Gly Cys Ile Ile Thr Ser Leu Thr Gly	
50 55 60	
CGG GAC AAG AAC CAG GTC GAG GGA GAG GTT CAG GTG GTT TCC ACC GCA	240

165

Arg 65	Asp	Lys	Asn	Gln	Val 70	Glu	Gly	Glu	Val	Gln 75	Val	Val	Ser	Thr	Ala 80	
ACA	CAA	TCC	TTC	CTG	GCG	ACC	TGC	GTC	AAC	GGC	GTG	TGT	TGG	ACC	GTT	288
Thr	Gln	Ser	Phe	Leu	Ala	Thr	Cys	Val	Asn 90	Gly	Val	Cys	Trp	Thr	Val	
				85										95		
TAC	CAT	GGT	GCT	GGC	TCA	AAG	ACC	TTA	GCC	GGC	CCA	AAG	GGG	CCA	ATC	336
Tyr	His	Gly	Ala	Gly	Ser	Lys	Thr	Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile	
			100					105					110			
ACC	CAG	ATG	TAC	ACT	AAT	GTG	GAC	CAG	GAC	CTC	GTC	GGC	TGG	CAG	GCG	384
Thr	Gln	Met	Tyr	Thr	Asn	Val	Asp	Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala	
		115					120					125				
CCC	CCC	GGG	GCG	CGT	TCC	TTG	ACA	CCA	TGC	ACC	TGT	GGC	AGC	TCA	GAC	432
Pro	Pro	Gly	Ala	Arg	Ser	Leu	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	
		130				135						140				
CTT	TAC	TTG	GTC	ACG	AGA	CAT	GCT	GAC	GTC	ATT	CCG	GTG	CGC	CGG	CGG	480
Leu	Tyr	Leu	Val	Thr	Arg	His	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	
145					150					155					160	
GGC	GAC	AGT	AGG	GGG	AGC	CTG	CTC	TCC	CCC	AGG	CCT	GTC	TCC	TAC	TTG	528
Gly	Asp	Ser	Arg	Gly	Ser	Leu	Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	
				165					170					175		
AAG	GGC	TCT	TCG	GGT	GGT	CCA	CTG	CTC	TGC	CCT	TCG	GGG	CAC	GCT	GTG	576
Lys	Gly	Ser	Ser	Gly	Gly	Pro	Leu	Leu	Cys	Pro	Ser	Gly	His	Ala	Val	
			180					185					190			
GGC	ATC	TTC	CGG	GCT	GCC	GTA	TGC	ACC	CGG	GGG	GTT	GCG	AAG	GCG	GTG	624
Gly	Ile	Phe	Arg	Ala	Ala	Val	Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	
		195					200					205				
GAC	TTT	GTG	CCC	GTA	GAG	TCC	ATG	GAA	ACT	ACT	ATG	CGG	TCT	CCG	GTC	672
Asp	Phe	Val	Pro	Val	Glu	Ser	Met	Glu	Thr	Thr	Met	Arg	Ser	Pro	Val	
	210					215					220					
TTC	ACG	GAC	AAC	TCA	TCC	CCC	CCG	GCC	GTA	CCG	CAG	TCA	TTT	CAA	GTG	720
Phe	Thr	Asp	Asn	Ser	Ser	Pro	Pro	Ala	Val	Pro	Gln	Ser	Phe	Gln	Val	
225					230					235					240	
GCC	CAC	CTA	CAC	GCT	CCC	ACT	GGC	AGC	GGC	AAG	AGT	ACT	AAA	GTG	CCG	768
Ala	His	Leu	His	Ala	Pro	Thr	Gly	Ser	Gly	Lys	Ser	Thr	Lys	Val	Pro	
				245					250					255		
GCT	GCA	TAT	GCA	GCC	CAA	GGG	TAC	AAG	GTG	CTC	GTC	CTC	AAT	CCG	TCC	816
Ala	Ala	Tyr	Ala	Ala	Gln	Gly	Tyr	Lys	Val	Leu	Val	Leu	Asn	Pro	Ser	
			260					265					270			
GTT	GCC	GCT	ACC	TTA	GGG	TTT	GGG	GCG	TAT	ATG	TCT	AAG	GCA	CAC	GGT	864
Val	Ala	Ala	Thr	Leu	Gly	Phe	Gly	Ala	Tyr	Met	Ser	Lys	Ala	His	Gly	
		275					280					285				
ATT	GAC	CCC	AAC	ATC	AGA	ACT	GGG	GTA	AGG	ACC	ATT	ACC	ACA	GGC	GCC	912
Ile	Asp	Pro	Asn	Ile	Arg	Thr	Gly	Val	Arg	Thr	Ile	Thr	Thr	Gly	Ala	
	290					295					300					

CCC	GTC	ACA	TAC	TCT	ACC	TAT	GGC	AAG	TTT	CTT	GCC	GAT	GGT	GGT	TGC	960
Pro	Val	Thr	Tyr	Ser	Thr	Tyr	Gly	Lys	Phe	Leu	Ala	Asp	Gly	Gly	Cys	
305					310					315					320	
TCT	GGG	GGC	GCT	TAT	GAC	ATC	ATA	ATA	TGT	GAT	GAG	TGC	CAT	TCA	ACT	1008
Ser	Gly	Gly	Ala	Tyr	Asp	Ile	Ile	Ile	Cys	Asp	Glu	Cys	His	Ser	Thr	
				325					330					335		
GAC	TCG	ACT	ACA	ATC	TTG	GGC	ATC	GGC	ACA	GTC	CTG	GAC	CAA	GCG	GAG	1056
Asp	Ser	Thr	Thr	Ile	Leu	Gly	Ile	Gly	Thr	Val	Leu	Asp	Gln	Ala	Glu	
			340					345					350			
ACG	GCT	GGA	GCG	CGG	CTT	GTC	GTG	CTC	GCC	ACC	GCT	ACG	CCT	CCG	GGA	1104
Thr	Ala	Gly	Ala	Arg	Leu	Val	Val	Leu	Ala	Thr	Ala	Thr	Pro	Pro	Gly	
		355				360					365					
TCG	GTC	ACC	GTG	CCA	CAC	CCA	AAC	ATC	GAG	GAG	GTG	GCC	CTG	TCT	AAT	1152
Ser	Val	Thr	Val	Pro	His	Pro	Asn	Ile	Glu	Glu	Val	Ala	Leu	Ser	Asn	
	370					375					380					
ACT	GGA	GAG	ATC	CCC	TTC	TAT	GGC	AAA	GCC	ATC	CCC	ATT	GAA	GCC	ATC	1200
Thr	Gly	Glu	Ile	Pro	Phe	Tyr	Gly	Lys	Ala	Ile	Pro	Ile	Glu	Ala	Ile	
385					390				395						400	
AGG	GGG	GGA	AGG	CAT	CTC	ATT	TTC	TGT	CAT	TCC	AAG	AAG	AAG	TGC	GAC	1248
Arg	Gly	Gly	Arg	His	Leu	Ile	Phe	Cys	His	Ser	Lys	Lys	Lys	Cys	Asp	
				405					410					415		
GAG	CTC	GCC	GCA	AAG	CTG	TCA	GGC	CTC	GGA	ATC	AAC	GCT	GTG	GCG	TAT	1296
Glu	Leu	Ala	Ala	Lys	Leu	Ser	Gly	Leu	Gly	Ile	Asn	Ala	Val	Ala	Tyr	
			420					425					430			
TAC	CGG	GGG	CTC	GAT	GTG	TCC	GTC	ATA	CCA	ACT	ATC	GGA	GAC	GTC	GTT	1344
Tyr	Arg	Gly	Leu	Asp	Val	Ser	Val	Ile	Pro	Thr	Ile	Gly	Asp	Val	Val	
		435					440					445				
GTC	GTG	GCA	ACA	GAC	GCT	CTG	ATG	ACG	GGC	TAT	ACG	GGC	GAC	TTT	GAC	1392
Val	Val	Ala	Thr	Asp	Ala	Leu	Met	Thr	Gly	Tyr	Thr	Gly	Asp	Phe	Asp	
	450					455					460					
TCA	GTG	ATC	GAC	TGT	AAC	ACA	TGT	GTC	ACC	CAG	ACA	GTC	GAC	TTC	AGC	1440
Ser	Val	Ile	Asp	Cys	Asn	Thr	Cys	Val	Thr	Gln	Thr	Val	Asp	Phe	Ser	
465					470					475					480	
TTG	GAT	CCC	ACC	TTC	ACC	ATT	GAG	ACG	ACG	ACC	GTG	CCT	CAA	GAC	GCA	1488
Leu	Asp	Pro	Thr	Phe	Thr	Ile	Glu	Thr	Thr	Thr	Val	Pro	Gln	Asp	Ala	
				485					490					495		
GTG	TCG	CGC	TCG	CAG	CGG	CGG	GGT	AGG	ACT	GGC	AGG	GGT	AGG	AGA	GGC	1536
Val	Ser	Arg	Ser	Gln	Arg	Arg	Gly	Arg	Thr	Gly	Arg	Gly	Arg	Arg	Gly	
			500					505					510			
ATC	TAC	AGG	TTT	GTG	ACT	CCG	GGA	GAA	CGG	CCC	TCG	GGC	ATG	TTC	GAT	1584
Ile	Tyr	Arg	Phe	Val	Thr	Pro	Gly	Glu	Arg	Pro	Ser	Gly	Met	Phe	Asp	
		515					520					525				
TCC	TCG	GTC	CTG	TGT	GAG	TGC	TAT	GAC	GCG	GGC	TGT	GCT	TGG	TAC	GAG	1632



Ser	Ser	Val	Leu	Cys	Glu	Cys	Tyr	Asp	Ala	Gly	Cys	Ala	Trp	Tyr	Glu	
530						535					540					
CTC	ACC	CCC	GCC	GAG	ACC	TCG	GTT	AGG	TTG	CGG	GCC	TAC	CTG	AAC	ACA	1680
Leu	Thr	Pro	Ala	Glu	Thr	Ser	Val	Arg	Leu	Arg	Ala	Tyr	Leu	Asn	Thr	
545					550					555					560	
CCA	GGG	TTG	CCC	GTT	TGC	CAG	GAC	CAC	CTG	GAG	TTC	TGG	GAG	AGT	GTC	1728
Pro	Gly	Leu	Pro	Val	Cys	Gln	Asp	His	Leu	Glu	Phe	Trp	Glu	Ser	Val	
				565					570					575		
TTC	ACA	GGC	CTC	ACC	CAT	ATA	GAT	GCA	CAC	TTC	TTG	TCC	CAG	ACC	AAG	1776
Phe	Thr	Gly	Leu	Thr	His	Ile	Asp	Ala	His	Phe	Leu	Ser	Gln	Thr	Lys	
			580					585					590			
CAG	GCA	GGA	GAC	AAC	TTC	CCC	TAC	CTG	GTA	GCA	TAC	CAA	GCC	ACG	GTG	1824
Gln	Ala	Gly	Asp	Asn	Phe	Pro	Tyr	Leu	Val	Ala	Tyr	Gln	Ala	Thr	Val	
		595					600					605				
TGC	GCC	AGG	GCT	CAG	GCC	CCA	CCT	CCA	TCA	TGG	GAT	CAA	ATG	TGG	AAG	1872
Cys	Ala	Arg	Ala	Gln	Ala	Pro	Pro	Pro	Ser	Trp	Asp	Gln	Met	Trp	Lys	
	610					615					620					
TGT	CTC	ATA	CGG	CTG	AAA	CCT	ACG	CTG	CAC	GGG	CCA	ACA	CCC	TTG	CTG	1920
Cys	Leu	Ile	Arg	Leu	Lys	Pro	Thr	Leu	His	Gly	Pro	Thr	Pro	Leu	Leu	
625					630					635					640	
TAC	AGG	CTG	GGA	GCC	GTC	CAA	AAT	GAG	GTC	ACC	CTC	ACC	CAC	CCC	ATA	1968
Tyr	Arg	Leu	Gly	Ala	Val	Gln	Asn	Glu	Val	Thr	Leu	Thr	His	Pro	Ile	
				645					650					655		
ACC	AAA	TAC	ATC	ATG	GCA	TGC	ATG	TCG	GCT	GAC	CTG	GAG	GTC	GTC	ACT	2016
Thr	Lys	Tyr	Ile	Met	Ala	Cys	Met	Ser	Ala	Asp	Leu	Glu	Val	Val	Thr	
			660					665					670			

## (2) INFORMATION FOR SEQ ID NO:111:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2016 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2016

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG 48

168

Met	Gly	Ser	Ser	His	His	His	His	His	His	Ser	Ser	Gly	Leu	Val	Pro	
1				5					10					15		
CGC	GGC	AGC	CAT	ATG	GCT	TAC	TCT	CTG	ACT	ACG	GGT	TCT	GTT	GTT	ATT	96
Arg	Gly	Ser	His	Met	Ala	Tyr	Ser	Leu	Thr	Thr	Gly	Ser	Val	Val	Ile	
			20					25					30			
GTT	GGT	AGA	ATT	ATT	TTA	TCT	GGT	AGT	GGT	AGT	ATC	ACG	GCC	TAC	TCC	144
Val	Gly	Arg	Ile	Ile	Leu	Ser	Gly	Ser	Gly	Ser	Ile	Thr	Ala	Tyr	Ser	
		35					40					45				
CAA	CAG	ACG	CGG	GGC	CTA	CTT	GGT	TGC	ATC	ATC	ACT	AGC	CTT	ACA	GGC	192
Gln	Gln	Thr	Arg	Gly	Leu	Leu	Gly	Cys	Ile	Ile	Thr	Ser	Leu	Thr	Gly	
	50					55					60					
CGG	GAC	AAG	AAC	CAG	GTC	GAG	GGA	GAG	GTT	CAG	GTG	GTT	TCC	ACC	GCA	240
Arg	Asp	Lys	Asn	Gln	Val	Glu	Gly	Glu	Val	Gln	Val	Val	Ser	Thr	Ala	
65					70					75					80	
ACA	CAA	TCC	TTC	CTG	GCG	ACC	TGC	GTC	AAC	GGC	GTG	TGT	TGG	ACC	GTT	288
Thr	Gln	Ser	Phe	Leu	Ala	Thr	Cys	Val	Asn	Gly	Val	Cys	Trp	Thr	Val	
				85					90					95		
TAC	CAT	GGT	GCT	GGC	TCA	AAG	ACC	TTA	GCC	GGC	CCA	AAG	GGG	CCA	ATC	336
Tyr	His	Gly	Ala	Gly	Ser	Lys	Thr	Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile	
			100					105					110			
ACC	CAG	ATG	TAC	ACT	AAT	GTG	GAC	CAG	GAC	CTC	GTC	GGC	TGG	CAG	GCG	384
Thr	Gln	Met	Tyr	Thr	Asn	Val	Asp	Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala	
		115					120					125				
CCC	CCC	GGG	GCG	CGT	TCC	TTG	ACA	CCA	TGC	ACC	TGT	GGC	AGC	TCA	GAC	432
Pro	Pro	Gly	Ala	Arg	Ser	Leu	Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	
	130					135					140					
CTT	TAC	TTG	GTC	ACG	AGA	CAT	GCT	GAC	GTC	ATT	CCG	GTG	CGC	CGG	CGG	480
Leu	Tyr	Leu	Val	Thr	Arg	His	Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	
145					150					155					160	
GGC	GAC	AGT	AGG	GGG	AGC	CTG	CTC	TCC	CCC	AGG	CCT	GTC	TCC	TAC	TTG	528
Gly	Asp	Ser	Arg	Gly	Ser	Leu	Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	
				165					170					175		
AAG	GGC	TCT	GCT	GGT	GGT	CCA	CTG	CTC	TGC	CCT	TCG	GGG	CAC	GCT	GTG	576
Lys	Gly	Ser	Ala	Gly	Gly	Pro	Leu	Leu	Cys	Pro	Ser	Gly	His	Ala	Val	
			180					185					190			
GGC	ATC	TTC	CGG	GCT	GCC	GTA	TGC	ACC	CGG	GGG	GTT	GCG	AAG	GCG	GTG	624
Gly	Ile	Phe	Arg	Ala	Ala	Val	Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	
		195					200					205				
GAC	TTT	GTG	CCC	GTA	GAG	TCC	ATG	GAA	ACT	ACT	ATG	CGG	TCT	CCG	GTC	672
Asp	Phe	Val	Pro	Val	Glu	Ser	Met	Glu	Thr	Thr	Met	Arg	Ser	Pro	Val	
	210					215					220					
TTC	ACG	GAC	AAC	TCA	TCC	CCC	CCG	GCC	GTA	CCG	CAG	TCA	TTT	CAA	GTG	720
Phe	Thr	Asp	Asn	Ser	Ser	Pro	Pro	Ala	Val	Pro	Gln	Ser	Phe	Gln	Val	
225					230					235					240	

GCC CAC CTA CAC GCT CCC ACT GGC AGC GGC AAG AGT ACT AAA GTG CCG	768
Ala His Leu His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys Val Pro	
245 250 255	
GCT GCA TAT GCA GCC CAA GGG TAC AAG GTG CTC GTC CTC AAT CCG TCC	816
Ala Ala Tyr Ala Ala Gln Gly Tyr Lys Val Leu Val Leu Asn Pro Ser	
260 265 270	
GTT GCC GCT ACC TTA GGG TTT GGG GCG TAT ATG TCT AAG GCA CAC GGT	864
Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr Met Ser Lys Ala His Gly	
275 280 285	
ATT GAC CCC AAC ATC AGA ACT GGG GTA AGG ACC ATT ACC ACA GGC GCC	912
Ile Asp Pro Asn Ile Arg Thr Gly Val Arg Thr Ile Thr Thr Gly Ala	
290 295 300	
CCC GTC ACA TAC TCT ACC TAT GGC AAG TTT CTT GCC GAT GGT GGT TGC	960
Pro Val Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala Asp Gly Gly Cys	
305 310 315 320	
TCT GGG GGC GCT TAT GAC ATC ATA ATA TGT GAT GAG TGC CAT TCA ACT	1008
Ser Gly Gly Ala Tyr Asp Ile Ile Ile Cys Asp Glu Cys His Ser Thr	
325 330 335	
GAC TCG ACT ACA ATC TTG GGC ATC GGC ACA GTC CTG GAC CAA GCG GAG	1056
Asp Ser Thr Thr Ile Leu Gly Ile Gly Thr Val Leu Asp Gln Ala Glu	
340 345 350	
ACG GCT GGA GCG CGG CTT GTC GTG CTC GCC ACC GCT ACG CCT CCG GGA	1104
Thr Ala Gly Ala Arg Leu Val Val Leu Ala Thr Ala Thr Pro Pro Gly	
355 360 365	
TCG GTC ACC GTG CCA CAC CCA AAC ATC GAG GAG GTG GCC CTG TCT AAT	1152
Ser Val Thr Val Pro His Pro Asn Ile Glu Glu Val Ala Leu Ser Asn	
370 375 380	
ACT GGA GAG ATC CCC TTC TAT GGC AAA GCC ATC CCC ATT GAA GCC ATC	1200
Thr Gly Glu Ile Pro Phe Tyr Gly Lys Ala Ile Pro Ile Glu Ala Ile	
385 390 395 400	
AGG GGG GGA AGG CAT CTC ATT TTC TGT CAT TCC AAG AAG AAG TGC GAC	1248
Arg Gly Gly Arg His Leu Ile Phe Cys His Ser Lys Lys Lys Cys Asp	
405 410 415	
GAG CTC GCC GCA AAG CTG TCA GGC CTC GGA ATC AAC GCT GTG GCG TAT	1296
Glu Leu Ala Ala Lys Leu Ser Gly Leu Gly Ile Asn Ala Val Ala Tyr	
420 425 430	
TAC CGG GGG CTC GAT GTG TCC GTC ATA CCA ACT ATC GGA GAC GTC GTT	1344
Tyr Arg Gly Leu Asp Val Ser Val Ile Pro Thr Ile Gly Asp Val Val	
435 440 445	
GTC GTG GCA ACA GAC GCT CTG ATG ACG GGC TAT ACG GGC GAC TTT GAC	1392
Val Val Ala Thr Asp Ala Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp	
450 455 460	
TCA GTG ATC GAC TGT AAC ACA TGT GTC ACC CAG ACA GTC GAC TTC AGC	1440

Ser 465	Val	Ile	Asp	Cys	Asn 470	Thr	Cys	Val	Thr	Gln 475	Thr	Val	Asp	Phe	Ser 480	
TTG	GAT	CCC	ACC	TTC	ACC	ATT	GAG	ACG	ACG	ACC	GTG	CCT	CAA	GAC	GCA	1488
Leu	Asp	Pro	Thr	Phe 485	Thr	Ile	Glu	Thr	Thr	Thr	Val	Pro	Gln	Asp 495	Ala	
GTG	TCG	CGC	TCG	CAG	CGG	CGG	GGT	AGG	ACT	GGC	AGG	GGT	AGG	AGA	GGC	1536
Val	Ser	Arg	Ser	Gln 500	Arg	Arg	Gly	Arg 505	Thr	Gly	Arg	Gly	Arg	Arg	Gly	
ATC	TAC	AGG	TTT	GTG	ACT	CCG	GGA	GAA	CGG	CCC	TCG	GGC	ATG	TTC	GAT	1584
Ile	Tyr	Arg	Phe 515	Val	Thr	Pro	Gly	Glu 520	Arg	Pro	Ser	Gly	Met	Phe	Asp	
TCC	TCG	GTC	CTG	TGT	GAG	TGC	TAT	GAC	GCG	GGC	TGT	GCT	TGG	TAC	GAG	1632
Ser	Ser	Val	Leu	Cys	Glu	Cys	Tyr	Asp 535	Ala	Gly	Cys	Ala	Trp	Tyr	Glu	
CTC	ACC	CCC	GCC	GAG	ACC	TCG	GTT	AGG	TTG	CGG	GCC	TAC	CTG	AAC	ACA	1680
Leu	Thr	Pro	Ala	Glu	Thr 550	Ser	Val	Arg	Leu	Arg	Ala	Tyr	Leu	Asn	Thr 560	
CCA	GGG	TTG	CCC	GTT	TGC	CAG	GAC	CAC	CTG	GAG	TTC	TGG	GAG	AGT	GTC	1728
Pro	Gly	Leu	Pro	Val 565	Cys	Gln	Asp	His 570	Leu	Glu	Phe	Trp	Glu	Ser	Val 575	
TTC	ACA	GGC	CTC	ACC	CAT	ATA	GAT	GCA	CAC	TTC	TTG	TCC	CAG	ACC	AAG	1776
Phe	Thr	Gly	Leu 580	Thr	His	Ile	Asp	Ala 585	His	Phe	Leu	Ser	Gln	Thr	Lys	
CAG	GCA	GGA	GAC	AAC	TTC	CCC	TAC	CTG	GTA	GCA	TAC	CAA	GCC	ACG	GTG	1824
Gln	Ala	Gly	Asp	Asn	Phe	Pro	Tyr	Leu 600	Val	Ala	Tyr	Gln	Ala	Thr	Val	
TGC	GCC	AGG	GCT	CAG	GCC	CCA	CCT	CCA	TCA	TGG	GAT	CAA	ATG	TGG	AAG	1872
Cys	Ala	Arg	Ala	Gln	Ala	Pro	Pro	Pro	Ser	Trp	Asp	Gln	Met	Trp	Lys	
TGT	CTC	ATA	CGG	CTG	AAA	CCT	ACG	CTG	CAC	GGG	CCA	ACA	CCC	TTG	CTG	1920
Cys	Leu	Ile	Arg	Leu	Lys 630	Pro	Thr	Leu	His	Gly	Pro	Thr	Pro	Leu	Leu 640	
TAC	AGG	CTG	GGA	GCC	GTC	CAA	AAT	GAG	GTC	ACC	CTC	ACC	CAC	CCC	ATA	1968
Tyr	Arg	Leu	Gly	Ala 645	Val	Gln	Asn	Glu	Val 650	Thr	Leu	Thr	His	Pro	Ile 655	
ACC	AAA	TAC	ATC	ATG	GCA	TGC	ATG	TCG	GCT	GAC	CTG	GAG	GTC	GTC	ACT	2016
Thr	Lys	Tyr	Ile	Met	Ala	Cys	Met	Ser 665	Ala	Asp	Leu	Glu	Val	Val	Thr 670	

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

171

- (A) LENGTH: 648 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG	48
Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro	
1 5 10 15	
CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA	96
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	
20 25 30	
TCT CCT GCT GGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA CTT	144
Ser Pro Ala Gly Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu	
35 40 45	
GGT TGC ATC ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC GAG	192
Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu	
50 55 60	
GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG ACC	240
Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr	
65 70 75 80	
TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA AAG	288
Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys	
85 90 95	
ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT GTG	336
Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val	
100 105 110	
GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC TTG	384
Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu	
115 120 125	
ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA CAT	432
Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His	
130 135 140	
GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC CTG	480
Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu	
145 150 155 160	
CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT CCA	528
Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro	
165 170 175	

172

CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC GTA	576
Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val	
180 185 190	
TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG TCC	624
Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser	
195 200 205	
ATG GAA ACT ACT ATG CGG TCT TGA	648
Met Glu Thr Thr Met Arg Ser	
210 215	

## (2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 648 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..648

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113

ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG	48
Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro	
1 5 10 15	
CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA	96
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	
20 25 30	
TCT CCT GCT GGT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA CTT	144
Ser Pro Ala Gly Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu	
35 40 45	
GGT TGC AAG ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC GAG	192
Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu	
50 55 60	
GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG ACC	240
Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr	
65 70 75 80	
TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA AAG	288
Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys	
85 90 95	
ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT GTG	336

Thr	Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	Val		
			100					105						110			
GAC	CAG	GAC	CTC	GTC	GGC	TGG	CAG	GCG	CCC	CCC	GGG	GCG	CGT	TCC	TTG	384	
Asp	Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	Leu		
		115					120					125					
ACA	CCA	TGC	ACC	TGT	GGC	AGC	TCA	GAC	CTT	TAC	TTG	GTC	ACG	AGA	CAT	432	
Thr	Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	His		
		130				135					140						
GCT	GAC	GTC	ATT	CCG	GTG	CGC	CGG	CGG	GGC	GAC	AGT	AGG	GGG	AGC	CTG	480	
Ala	Asp	Val	Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	Leu		
145					150					155					160		
CTC	TCC	CCC	AGG	CCT	GTC	TCC	TAC	TTG	AAG	GGC	TCT	TCG	GGT	GGT	CCA	528	
Leu	Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly	Pro		
				165					170						175		
CTG	CTC	TGC	CCT	TCG	GGG	CAC	GCT	GTG	GGC	ATC	TTC	CGG	GCT	GCC	GTA	576	
Leu	Leu	Cys	Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	Val		
			180					185					190				
TGC	ACC	CGG	GGG	GTT	GCG	AAG	GCG	GTG	GAC	TTT	GTG	CCC	GTA	GAG	TCC	624	
Cys	Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	Ser		
		195				200						205					
ATG	GAA	ACT	ACT	ATG	CGG	TCT	TGA									648	
Met	Glu	Thr	Thr	Met	Arg	Ser											
		210				215											

## (2) INFORMATION FOR SEQ ID NO:114:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 648 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..648

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

ATG	GGC	AGC	AGC	CAT	CAT	CAT	CAT	CAT	CAC	AGC	AGC	GGC	CTG	GTG	CCG	48	
Met	Gly	Ser	Ser	His	His	His	His	His	His	Ser	Ser	Gly	Leu	Val	Pro		
1				5					10					15			
CGC	GGC	AGC	CAT	ATG	GGT	TCT	GTT	GTT	ATT	GTT	GGT	AGA	ATT	ATT	TTA	96	
Arg	Gly	Ser	His	Met	Gly	Ser	Val	Val	Ile	Val	Gly	Arg	Ile	Ile	Leu		
			20					25					30				

174

TCT GGT GGT TCT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA CTT	144
Ser Gly Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu	
35 40 45	
GGT TGC ATC ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC GAG	192
Gly Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu	
50 55 60	
GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG ACC	240
Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr	
65 70 75 80	
TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA AAG	288
Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys	
85 90 95	
ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT GTG	336
Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val	
100 105 110	
GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC TTG	384
Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu	
115 120 125	
ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA CAT	432
Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His	
130 135 140	
GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC CTG	480
Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu	
145 150 155 160	
CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT CCA	528
Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro	
165 170 175	
CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC GTA	576
Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val	
180 185 190	
TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG TCC	624
Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser	
195 200 205	
ATG GAA ACT ACT ATG CGG TCT TGA	648
Met Glu Thr Thr Met Arg Ser	
210 215	

## (2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 648 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

175



## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..648

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC GGC CTG GTG CCG	48
Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro	
1 5 10 15	
CGC GGC AGC CAT ATG GGT TCT GTT GTT ATT GTT GGT AGA ATT ATT TTA	96
Arg Gly Ser His Met Gly Ser Val Val Ile Val Gly Arg Ile Ile Leu	
20 25 30	
TCT GGT GGT TCT ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA CTT	144
Ser Gly Gly Ser Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu	
35 40 45	
GGT TGC AAG ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC GAG	192
Gly Cys Lys Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu	
50 55 60	
GGA GAG GTT CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG ACC	240
Gly Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr	
65 70 75 80	
TGC GTC AAC GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA AAG	288
Cys Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys	
85 90 95	
ACC TTA GCC GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT GTG	336
Thr Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val	
100 105 110	
GAC CAG GAC CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC TTG	384
Asp Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu	
115 120 125	
ACA CCA TGC ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA CAT	432
Thr Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His	
130 135 140	
GCT GAC GTC ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC CTG	480
Ala Asp Val Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu	
145 150 155 160	
CTC TCC CCC AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT CCA	528
Leu Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro	
165 170 175	
CTG CTC TGC CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC GTA	576
Leu Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val	
180 185 190	
TGC ACC CGG GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTA GAG TCC	624

Cys Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser  
 195 200 205

ATG GAA ACT ACT ATG CGG TCT TGA  
 Met Glu Thr Thr Met Arg Ser  
 210 215

648

## (2) INFORMATION FOR SEQ ID NO:116:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1941 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1941

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

ATG CAT ATG CAT CAT CAT CAC CAT CAT CTG GTG CCG CGC GGC AGC GCG	48
Met His Met His His His His His His Leu Val Pro Arg Gly Ser Ala	
1 5 10 15	
CCC ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA CTT GGT TGC AAG	96
Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly Cys Lys	
20 25 30	
ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC GAG GGA GAG GTT	144
Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly Glu Val	
35 40 45	
CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG ACC TGC GTC AAC	192
Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys Val Asn	
50 55 60	
GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA AAG ACC TTA GCC	240
Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr Leu Ala	
65 70 75 80	
GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT GTG GAC CAG GAC	288
Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp Gln Asp	
85 90 95	
CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC TTG ACA CCA TGC	336
Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys	
100 105 110	
ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA CAT GCT GAC GTC	384
Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala Asp Val	
115 120 125	

ATT	CCG	GTG	CGC	CGG	CGG	GGC	GAC	AGT	AGG	GGG	AGC	CTG	CTC	TCC	CCC	432
Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	Leu	Leu	Ser	Pro	
	130					135					140					
AGG	CCT	GTC	TCC	TAC	TTG	AAG	GGC	TCT	TCG	GGT	GGT	CCA	CTG	CTC	TGC	480
Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly	Pro	Leu	Leu	Cys	
145					150					155					160	
CCT	TCG	GGG	CAC	GCT	GTG	GGC	ATC	TTC	CGG	GCT	GCC	GTA	TGC	ACC	CGG	528
Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	Val	Cys	Thr	Arg	
				165					170					175		
GGG	GTT	GCG	AAG	GCG	GTG	GAC	TTT	GTG	CCC	GTA	GAG	TCC	ATG	GAA	ACT	576
Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	Ser	Met	Glu	Thr	
			180					185					190			
ACT	ATG	CGG	TCT	CCG	GTC	TTC	ACG	GAC	AAC	TCA	TCC	CCC	CCG	GCC	GTA	624
Thr	Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser	Ser	Pro	Pro	Ala	Val	
		195					200					205				
CCG	CAG	TCA	TTT	CAA	GTG	GCC	CAC	CTA	CAC	GCT	CCC	ACT	GGC	AGC	GGC	672
Pro	Gln	Ser	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro	Thr	Gly	Ser	Gly	
	210					215					220					
AAG	AGT	ACT	AAA	GTG	CCG	GCT	GCA	TAT	GCA	GCC	CAA	GGG	TAC	AAG	GTG	720
Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	Gly	Tyr	Lys	Val	
225					230					235					240	
CTC	GTC	CTC	AAT	CCG	TCC	GTT	GCC	GCT	ACC	TTA	GGG	TTT	GGG	GCG	TAT	768
Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly	Phe	Gly	Ala	Tyr	
				245					250					255		
ATG	TCT	AAG	GCA	CAC	GGT	ATT	GAC	CCC	AAC	ATC	AGA	ACT	GGG	GTA	AGG	816
Met	Ser	Lys	Ala	His	Gly	Ile	Asp	Pro	Asn	Ile	Arg	Thr	Gly	Val	Arg	
			260				265						270			
ACC	ATT	ACC	ACA	GGC	GCC	CCC	GTC	ACA	TAC	TCT	ACC	TAT	GGC	AAG	TTT	864
Thr	Ile	Thr	Thr	Gly	Ala	Pro	Val	Thr	Tyr	Ser	Thr	Tyr	Gly	Lys	Phe	
		275					280					285				
CTT	GCC	GAT	GGT	GGT	TGC	TCT	GGG	GGC	GCT	TAT	GAC	ATC	ATA	ATA	TGT	912
Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	Ile	Ile	Ile	Cys	
	290					295					300					
GAT	GAG	TGC	CAT	TCA	ACT	GAC	TCG	ACT	ACA	ATC	TTG	GGC	ATC	GGC	ACA	960
Asp	Glu	Cys	His	Ser	Thr	Asp	Ser	Thr	Thr	Ile	Leu	Gly	Ile	Gly	Thr	
305					310					315					320	
GTC	CTG	GAC	CAA	GCG	GAG	ACG	GCT	GGA	GCG	CGG	CTT	GTC	GTG	CTC	GCC	1008
Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	Val	Val	Leu	Ala	
				325					330					335		
ACC	GCT	ACG	CCT	CCG	GGA	TCG	GTC	ACC	GTG	CCA	CAC	CCA	AAC	ATC	GAG	1056
Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Val	Pro	His	Pro	Asn	Ile	Glu	
			340					345					350			
GAG	GTG	GCC	CTG	TCT	AAT	ACT	GGA	GAG	ATC	CCC	TTC	TAT	GGC	AAA	GCC	1104
Glu	Val	Ala	Leu	Ser	Asn	Thr	Gly	Glu	Ile	Pro	Phe	Tyr	Gly	Lys	Ala	

355					360					365						
ATC Ile	CCC Pro 370	ATT Ile	GAA Glu	GCC Ala	ATC Ile	AGG Arg 375	GGG Gly	GGA Gly	AGG Arg	CAT His	CTC Leu 380	ATT Ile	TTC Phe	TGT Cys	CAT His	1152
TCC Ser 385	AAG Lys	AAG Lys	AAG Lys	TGC Cys	GAC Asp 390	GAG Glu	CTC Leu	GCC Ala	GCA Ala	AAG Lys 395	CTG Leu	TCA Ser	GGC Gly	CTC Leu	GGA Gly 400	1200
ATC Ile	AAC Asn	GCT Ala	GTG Val	GCG Ala 405	TAT Tyr	TAC Tyr	CGG Arg	GGG Gly	CTC Leu 410	GAT Asp	GTG Val	TCC Ser	GTC Val	ATA Ile 415	CCA Pro	1248
ACT Thr	ATC Ile	GGA Gly	GAC Asp 420	GTC Val	GTT Val	GTC Val	GTG Val	GCA Ala 425	ACA Thr	GAC Asp	GCT Ala	CTG Leu	ATG Met 430	ACG Thr	GGC Gly	1296
TAT Tyr	ACG Thr	GGC Gly 435	GAC Asp	TTT Phe	GAC Asp	TCA Ser	GTG Val 440	ATC Ile	GAC Asp	TGT Cys	AAC Asn	ACA Thr 445	TGT Cys	GTC Val	ACC Thr	1344
CAG Gln 450	ACA Thr	GTC Val	GAC Asp	TTC Phe	AGC Ser	TTG Leu 455	GAT Asp	CCC Pro	ACC Thr	TTC Phe	ACC Thr 460	ATT Ile	GAG Glu	ACG Thr	ACG Thr	1392
ACC Thr 465	GTG Val	CCT Pro	CAA Gln	GAC Asp	GCA Ala 470	GTG Val	TCG Ser	CGC Arg	TCG Ser	CAG Gln 475	CGG Arg	CGG Arg	GGT Gly	AGG Arg	ACT Thr 480	1440
GGC Gly	AGG Arg	GGT Gly	AGG Arg	AGA Arg 485	GGC Gly	ATC Ile	TAC Tyr	AGG Arg	TTT Phe 490	GTG Val	ACT Thr	CCG Pro	GGA Gly	GAA Glu 495	CGG Arg	1488
CCC Pro	TCG Ser	GGC Gly	ATG Met 500	TTC Phe	GAT Asp	TCC Ser	TCG Ser	GTC Val 505	CTG Leu	TGT Cys	GAG Glu	TGC Cys	TAT Tyr 510	GAC Asp	GCG Ala	1536
GGC Gly	TGT Cys	GCT Ala 515	TGG Trp	TAC Tyr	GAG Glu	CTC Leu	ACC Thr 520	CCC Pro	GCC Ala	GAG Glu	ACC Thr 525	TCG Ser	GTT Val	AGG Arg	TTG Leu	1584
CGG Arg 530	GCC Ala	TAC Tyr	CTG Leu	AAC Asn	ACA Thr	CCA Pro 535	GGG Gly	TTG Leu	CCC Pro	GTT Val	TGC Cys 540	CAG Gln	GAC Asp	CAC His	CTG Leu	1632
GAG Glu 545	TTC Phe	TGG Trp	GAG Glu	AGT Ser	GTC Val 550	TTC Phe	ACA Thr	GGC Gly	CTC Leu	ACC Thr 555	CAT His	ATA Ile	GAT Asp	GCA Ala	CAC His 560	1680
TTC Phe	TTG Leu	TCC Ser	CAG Gln	ACC Thr 565	AAG Lys	CAG Gln	GCA Ala	GGA Gly	GAC Asp 570	AAC Asn	TTC Phe	CCC Pro	TAC Tyr	CTG Leu 575	GTA Val	1728
GCA Ala	TAC Tyr	CAA Gln	GCC Ala 580	ACG Thr	GTG Val	TGC Cys	GCC Ala	AGG Arg 585	GCT Ala	CAG Gln	GCC Ala	CCA Pro	CCT Pro 590	CCA Pro	TCA Ser	1776

TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA CCT ACG CTG CAC	1824
Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His	
595 600 605	
GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC CAA AAT GAG GTC	1872
Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Val	
610 615 620	
ACC CTC ACC CAC CCC ATA ACC AAA TAC ATC ATG GCA TGC ATG TCG GCC	1920
Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala	
625 630 635 640	
GAC CTG GAG GTC GTT ACG TAG	1941
Asp Leu Glu Val Val Thr	
645	

## (2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1941 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1941

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

ATG CAT ATG CAT CAT CAT CAC CAT CAT CTG GTG CCG CGC GGC AGC GCG	48
Met His Met His His His His His Leu Val Pro Arg Gly Ser Ala	
1 5 10 15	
CCC ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA CTT GGT TGC ATC	96
Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile	
20 25 30	
AAG ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC GAG GGA GAG GTT	144
Lys Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly Glu Val	
35 40 45	
CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG ACC TGC GTC AAC	192
Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys Val Asn	
50 55 60	
GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA AAG ACC TTA GCC	240
Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr Leu Ala	
65 70 75 80	
GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT GTG GAC CAG GAC	288

180

Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	Val	Asp	Gln	Asp	
				85					90					95		
CTC	GTC	GGC	TGG	CAG	GCG	CCC	CCC	GGG	GCG	CGT	TCC	TTG	ACA	CCA	TGC	336
Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	Leu	Thr	Pro	Cys	
			100					105					110			
ACC	TGT	GGC	AGC	TCA	GAC	CTT	TAC	TTG	GTC	ACG	AGA	CAT	GCT	GAC	GTC	384
Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	His	Ala	Asp	Val	
		115					120					125				
ATT	CCG	GTG	CGC	CGG	CGG	GGC	GAC	AGT	AGG	GGG	AGC	CTG	CTC	TCC	CCC	432
Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	Leu	Leu	Ser	Pro	
	130					135					140					
AGG	CCT	GTC	TCC	TAC	TTG	AAG	GGC	TCT	TCG	GGT	GGT	CCA	CTG	CTC	TGC	480
Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly	Pro	Leu	Leu	Cys	
145					150					155					160	
CCT	TCG	GGG	CAC	GCT	GTG	GGC	ATC	TTC	CGG	GCT	GCC	GTA	TGC	ACC	CGG	528
Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	Val	Cys	Thr	Arg	
				165					170					175		
GGG	GTT	GCG	AAG	GCG	GTG	GAC	TTT	GTG	CCC	GTA	GAG	TCC	ATG	GAA	ACT	576
Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	Ser	Met	Glu	Thr	
			180					185					190			
ACT	ATG	CGG	TCT	CCG	GTC	TTC	ACG	GAC	AAC	TCA	TCC	CCC	CCG	GCC	GTA	624
Thr	Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser	Ser	Pro	Pro	Ala	Val	
		195					200					205				
CCG	CAG	TCA	TTT	CAA	GTG	GCC	CAC	CTA	CAC	GCT	CCC	ACT	GGC	AGC	GGC	672
Pro	Gln	Ser	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro	Thr	Gly	Ser	Gly	
	210					215					220					
AAG	AGT	ACT	AAA	GTG	CCG	GCT	GCA	TAT	GCA	GCC	CAA	GGG	TAC	AAG	GTG	720
Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	Gly	Tyr	Lys	Val	
225					230					235					240	
CTC	GTC	CTC	AAT	CCG	TCC	GTT	GCC	GCT	ACC	TTA	GGG	TTT	GGG	GCG	TAT	768
Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly	Phe	Gly	Ala	Tyr	
				245					250					255		
ATG	TCT	AAG	GCA	CAC	GGT	ATT	GAC	CCC	AAC	ATC	AGA	ACT	GGG	GTA	AGG	816
Met	Ser	Lys	Ala	His	Gly	Ile	Asp	Pro	Asn	Ile	Arg	Thr	Gly	Val	Arg	
			260				265						270			
ACC	ATT	ACC	ACA	GGC	GCC	CCC	GTC	ACA	TAC	TCT	ACC	TAT	GGC	AAG	TTT	864
Thr	Ile	Thr	Thr	Gly	Ala	Pro	Val	Thr	Tyr	Ser	Thr	Tyr	Gly	Lys	Phe	
		275					280					285				
CTT	GCC	GAT	GGT	GGT	TGC	TCT	GGG	GGC	GCT	TAT	GAC	ATC	ATA	ATA	TGT	912
Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	Ile	Ile	Ile	Cys	
	290					295					300					
GAT	GAG	TGC	CAT	TCA	ACT	GAC	TCG	ACT	ACA	ATC	TTG	GGC	ATC	GGC	ACA	960
Asp	Glu	Cys	His	Ser	Thr	Asp	Ser	Thr	Thr	Ile	Leu	Gly	Ile	Gly	Thr	
305					310					315					320	

GTC	CTG	GAC	CAA	GCG	GAG	ACG	GCT	GGA	GCG	CGG	CTT	GTC	GTG	CTC	GCC	1008
Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	Val	Val	Leu	Ala	
				325					330					335		
ACC	GCT	ACG	CCT	CCG	GGA	TCG	GTC	ACC	GTG	CCA	CAC	CCA	AAC	ATC	GAG	1056
Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Val	Pro	His	Pro	Asn	Ile	Glu	
			340					345					350			
GAG	GTG	GCC	CTG	TCT	AAT	ACT	GGA	GAG	ATC	CCC	TTC	TAT	GGC	AAA	GCC	1104
Glu	Val	Ala	Leu	Ser	Asn	Thr	Gly	Glu	Ile	Pro	Phe	Tyr	Gly	Lys	Ala	
		355					360					365				
ATC	CCC	ATT	GAA	GCC	ATC	AGG	GGG	GGA	AGG	CAT	CTC	ATT	TTC	TGT	CAT	1152
Ile	Pro	Ile	Glu	Ala	Ile	Arg	Gly	Gly	Arg	His	Leu	Ile	Phe	Cys	His	
	370					375					380					
TCC	AAG	AAG	AAG	TGC	GAC	GAG	CTC	GCC	GCA	AAG	CTG	TCA	GGC	CTC	GGA	1200
Ser	Lys	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Ala	Lys	Leu	Ser	Gly	Leu	Gly	
385					390					395					400	
ATC	AAC	GCT	GTG	GCG	TAT	TAC	CGG	GGG	CTC	GAT	GTG	TCC	GTC	ATA	CCA	1248
Ile	Asn	Ala	Val	Ala	Tyr	Tyr	Arg	Gly	Leu	Asp	Val	Ser	Val	Ile	Pro	
				405					410					415		
ACT	ATC	GGA	GAC	GTC	GTT	GTC	GTG	GCA	ACA	GAC	GCT	CTG	ATG	ACG	GGC	1296
Thr	Ile	Gly	Asp	Val	Val	Val	Val	Ala	Thr	Asp	Ala	Leu	Met	Thr	Gly	
			420					425					430			
TAT	ACG	GGC	GAC	TTT	GAC	TCA	GTG	ATC	GAC	TGT	AAC	ACA	TGT	GTC	ACC	1344
Tyr	Thr	Gly	Asp	Phe	Asp	Ser	Val	Ile	Asp	Cys	Asn	Thr	Cys	Val	Thr	
		435					440					445				
CAG	ACA	GTC	GAC	TTC	AGC	TTG	GAT	CCC	ACC	TTC	ACC	ATT	GAG	ACG	ACG	1392
Gln	Thr	Val	Asp	Phe	Ser	Leu	Asp	Pro	Thr	Phe	Thr	Ile	Glu	Thr	Thr	
	450					455					460					
ACC	GTG	CCT	CAA	GAC	GCA	GTG	TCG	CGC	TCG	CAG	CGG	CGG	GGT	AGG	ACT	1440
Thr	Val	Pro	Gln	Asp	Ala	Val	Ser	Arg	Ser	Gln	Arg	Arg	Gly	Arg	Thr	
465					470					475					480	
GGC	AGG	GGT	AGG	AGA	GGC	ATC	TAC	AGG	TTT	GTG	ACT	CCG	GGA	GAA	CGG	1488
Gly	Arg	Gly	Arg	Arg	Gly	Ile	Tyr	Arg	Phe	Val	Thr	Pro	Gly	Glu	Arg	
				485				490						495		
CCC	TCG	GGC	ATG	TTC	GAT	TCC	TCG	GTC	CTG	TGT	GAG	TGC	TAT	GAC	GCG	1536
Pro	Ser	Gly	Met	Phe	Asp	Ser	Ser	Val	Leu	Cys	Glu	Cys	Tyr	Asp	Ala	
			500					505					510			
GGC	TGT	GCT	TGG	TAC	GAG	CTC	ACC	CCC	GCC	GAG	ACC	TCG	GTT	AGG	TTG	1584
Gly	Cys	Ala	Trp	Tyr	Glu	Leu	Thr	Pro	Ala	Glu	Thr	Ser	Val	Arg	Leu	
		515					520					525				
CGG	GCC	TAC	CTG	AAC	ACA	CCA	GGG	TTG	CCC	GTT	TGC	CAG	GAC	CAC	CTG	1632
Arg	Ala	Tyr	Leu	Asn	Thr	Pro	Gly	Leu	Pro	Val	Cys	Gln	Asp	His	Leu	
	530					535					540					
GAG	TTC	TGG	GAG	AGT	GTC	TTC	ACA	GGC	CTC	ACC	CAT	ATA	GAT	GCA	CAC	1680

Glu	Phe	Trp	Glu	Ser	Val	Phe	Thr	Gly	Leu	Thr	His	Ile	Asp	Ala	His		
545					550					555					560		
TTC	TTG	TCC	CAG	ACC	AAG	CAG	GCA	GGA	GAC	AAC	TTC	CCC	TAC	CTG	GTA	1728	
Phe	Leu	Ser	Gln	Thr	Lys	Gln	Ala	Gly	Asp	Asn	Phe	Pro	Tyr	Leu	Val		
				565					570					575			
GCA	TAC	CAA	GCC	ACG	GTG	TGC	GCC	AGG	GCT	CAG	GCC	CCA	CCT	CCA	TCA	1776	
Ala	Tyr	Gln	Ala	Thr	Val	Cys	Ala	Arg	Ala	Gln	Ala	Pro	Pro	Pro	Ser		
			580					585					590				
TGG	GAT	CAA	ATG	TGG	AAG	TGT	CTC	ATA	CGG	CTG	AAA	CCT	ACG	CTG	CAC	1824	
Trp	Asp	Gln	Met	Trp	Lys	Cys	Leu	Ile	Arg	Leu	Lys	Pro	Thr	Leu	His		
		595					600					605					
GGG	CCA	ACA	CCC	TTG	CTG	TAC	AGG	CTG	GGA	GCC	GTC	CAA	AAT	GAG	GTC	1872	
Gly	Pro	Thr	Pro	Leu	Leu	Tyr	Arg	Leu	Gly	Ala	Val	Gln	Asn	Glu	Val		
	610					615					620						
ACC	CTC	ACC	CAC	CCC	ATA	ACC	AAA	TAC	ATC	ATG	GCA	TGC	ATG	TCG	GCC	1920	
Thr	Leu	Thr	His	Pro	Ile	Thr	Lys	Tyr	Ile	Met	Ala	Cys	Met	Ser	Ala		
	625				630					635					640		
GAC	CTG	GAG	GTC	GTT	ACG	TAG										1941	
Asp	Leu	Glu	Val	Val	Thr												
				645													

## (2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1941 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
- (A) NAME/KEY: CDS
  - (B) LOCATION: 1..1941

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

ATG	CAT	ATG	CAT	CAT	CAT	CAC	CAT	CAT	CTG	GTG	CCG	CGC	GGC	AGC	GCG	48	
Met	His	Met	His	His	His	His	His	His	Leu	Val	Pro	Arg	Gly	Ser	Ala		
1				5					10					15			
CCC	ATC	ACG	GCC	TAC	TCC	CAA	CAG	ACG	CGG	GGC	CTA	CTT	GGT	TGC	ATC	96	
Pro	Ile	Thr	Ala	Tyr	Ser	Gln	Gln	Thr	Arg	Gly	Leu	Leu	Gly	Cys	Ile		
			20					25					30				
ATC	ACT	AGC	CTT	ACA	GGC	CGG	GAC	AAG	AAC	CAG	GTC	GAG	GGA	GAG	GTT	144	
Ile	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val	Glu	Gly	Glu	Val		
			35				40						45				



CAG	GTG	GTT	TCC	ACC	GCA	ACA	CAA	TCC	TTC	CTG	GCG	ACC	TGC	GTC	AAC	192
Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala	Thr	Cys	Val	Asn	
	50						55					60				
GGC	GTG	TGT	TGG	ACC	GTT	TAC	CAT	GGT	GCT	GGC	TCA	AAG	ACC	TTA	GCC	240
Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser	Lys	Thr	Leu	Ala	
	65					70				75					80	
GGC	CCA	AAG	GGG	CCA	ATC	ACC	CAG	ATG	TAC	ACT	AAT	GTG	GAC	CAG	GAC	288
Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	Val	Asp	Gln	Asp	
				85					90					95		
CTC	GTC	GGC	TGG	CAG	GCG	CCC	CCC	GGG	GCG	CGT	TCC	TTG	ACA	CCA	TGC	336
Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	Leu	Thr	Pro	Cys	
			100					105					110			
ACC	TGT	GGC	AGC	TCA	GAC	CTT	TAC	TTG	GTC	ACG	AGA	CAT	GCT	GAC	GTC	384
Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	His	Ala	Asp	Val	
		115					120					125				
ATT	CCG	GTG	CGC	CGG	CGG	GGC	GAC	AGT	AGG	GGG	AGC	CTG	CTC	TCC	CCC	432
Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	Leu	Leu	Ser	Pro	
	130					135						140				
AGG	CCT	GTC	TCC	TAC	TTG	AAG	GGC	TCT	GCT	GGT	GGT	CCA	CTG	CTC	TGC	480
Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ala	Gly	Gly	Pro	Leu	Leu	Cys	
	145					150				155					160	
CCT	TCG	GGG	CAC	GCT	GTG	GGC	ATC	TTC	CGG	GCT	GCC	GTA	TGC	ACC	CGG	528
Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	Val	Cys	Thr	Arg	
				165					170					175		
GGG	GTT	GCG	AAG	GCG	GTG	GAC	TTT	GTG	CCC	GTA	GAG	TCC	ATG	GAA	ACT	576
Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	Ser	Met	Glu	Thr	
			180					185					190			
ACT	ATG	CGG	TCT	CCG	GTC	TTC	ACG	GAC	AAC	TCA	TCC	CCC	CCG	GCC	GTA	624
Thr	Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser	Ser	Pro	Pro	Ala	Val	
		195					200					205				
CCG	CAG	TCA	TTT	CAA	GTG	GCC	CAC	CTA	CAC	GCT	CCC	ACT	GGC	AGC	GGC	672
Pro	Gln	Ser	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro	Thr	Gly	Ser	Gly	
	210					215					220					
AAG	AGT	ACT	AAA	GTG	CCG	GCT	GCA	TAT	GCA	GCC	CAA	GGG	TAC	AAG	GTG	720
Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	Gly	Tyr	Lys	Val	
	225				230					235					240	
CTC	GTC	CTC	AAT	CCG	TCC	GTT	GCC	GCT	ACC	TTA	GGG	TTT	GGG	GCG	TAT	768
Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly	Phe	Gly	Ala	Tyr	
				245					250					255		
ATG	TCT	AAG	GCA	CAC	GGT	ATT	GAC	CCC	AAC	ATC	AGA	ACT	GGG	GTA	AGG	816
Met	Ser	Lys	Ala	His	Gly	Ile	Asp	Pro	Asn	Ile	Arg	Thr	Gly	Val	Arg	
			260					265					270			
ACC	ATT	ACC	ACA	GGC	GCC	CCC	GTC	ACA	TAC	TCT	ACC	TAT	GGC	AAG	TTT	864

Thr	Ile	Thr	Thr	Gly	Ala	Pro	Val	Thr	Tyr	Ser	Thr	Tyr	Gly	Lys	Phe	
	275						280					285				
CTT	GCC	GAT	GGT	GGT	TGC	TCT	GGG	GGC	GCT	TAT	GAC	ATC	ATA	ATA	TGT	912
Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	Ile	Ile	Ile	Cys	
	290					295				300						
GAT	GAG	TGC	CAT	TCA	ACT	GAC	TCG	ACT	ACA	ATC	TTG	GGC	ATC	GGC	ACA	960
Asp	Glu	Cys	His	Ser	Thr	Asp	Ser	Thr	Thr	Ile	Leu	Gly	Ile	Gly	Thr	
305					310					315					320	
GTC	CTG	GAC	CAA	GCG	GAG	ACG	GCT	GGA	GCG	CGG	CTT	GTC	GTG	CTC	GCC	1008
Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	Val	Val	Leu	Ala	
				325					330					335		
ACC	GCT	ACG	CCT	CCG	GGA	TCG	GTC	ACC	GTG	CCA	CAC	CCA	AAC	ATC	GAG	1056
Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Val	Pro	His	Pro	Asn	Ile	Glu	
			340					345					350			
GAG	GTG	GCC	CTG	TCT	AAT	ACT	GGA	GAG	ATC	CCC	TTC	TAT	GGC	AAA	GCC	1104
Glu	Val	Ala	Leu	Ser	Asn	Thr	Gly	Glu	Ile	Pro	Phe	Tyr	Gly	Lys	Ala	
	355						360					365				
ATC	CCC	ATT	GAA	GCC	ATC	AGG	GGG	GGA	AGG	CAT	CTC	ATT	TTC	TGT	CAT	1152
Ile	Pro	Ile	Glu	Ala	Ile	Arg	Gly	Gly	Arg	His	Leu	Ile	Phe	Cys	His	
	370					375					380					
TCC	AAG	AAG	AAG	TGC	GAC	GAG	CTC	GCC	GCA	AAG	CTG	TCA	GGC	CTC	GGA	1200
Ser	Lys	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Ala	Lys	Leu	Ser	Gly	Leu	Gly	
385					390					395					400	
ATC	AAC	GCT	GTG	GCG	TAT	TAC	CGG	GGG	CTC	GAT	GTG	TCC	GTC	ATA	CCA	1248
Ile	Asn	Ala	Val	Ala	Tyr	Tyr	Arg	Gly	Leu	Asp	Val	Ser	Val	Ile	Pro	
				405					410					415		
ACT	ATC	GGA	GAC	GTC	GTT	GTC	GTG	GCA	ACA	GAC	GCT	CTG	ATG	ACG	GGC	1296
Thr	Ile	Gly	Asp	Val	Val	Val	Val	Ala	Thr	Asp	Ala	Leu	Met	Thr	Gly	
			420					425					430			
TAT	ACG	GGC	GAC	TTT	GAC	TCA	GTG	ATC	GAC	TGT	AAC	ACA	TGT	GTC	ACC	1344
Tyr	Thr	Gly	Asp	Phe	Asp	Ser	Val	Ile	Asp	Cys	Asn	Thr	Cys	Val	Thr	
	435						440					445				
CAG	ACA	GTC	GAC	TTC	AGC	TTG	GAT	CCC	ACC	TTC	ACC	ATT	GAG	ACG	ACG	1392
Gln	Thr	Val	Asp	Phe	Ser	Leu	Asp	Pro	Thr	Phe	Thr	Ile	Glu	Thr	Thr	
	450					455						460				
ACC	GTG	CCT	CAA	GAC	GCA	GTG	TCG	CGC	TCG	CAG	CGG	CGG	GGT	AGG	ACT	1440
Thr	Val	Pro	Gln	Asp	Ala	Val	Ser	Arg	Ser	Gln	Arg	Arg	Gly	Arg	Thr	
465					470					475					480	
GGC	AGG	GGT	AGG	AGA	GGC	ATC	TAC	AGG	TTT	GTG	ACT	CCG	GGA	GAA	CGG	1488
Gly	Arg	Gly	Arg	Arg	Gly	Ile	Tyr	Arg	Phe	Val	Thr	Pro	Gly	Glu	Arg	
				485				490						495		
CCC	TCG	GGC	ATG	TTC	GAT	TCC	TCG	GTC	CTG	TGT	GAG	TGC	TAT	GAC	GCG	1536
Pro	Ser	Gly	Met	Phe	Asp	Ser	Ser	Val	Leu	Cys	Glu	Cys	Tyr	Asp	Ala	
			500					505					510			

GGC TGT GCT TGG TAC GAG CTC ACC CCC GCC GAG ACC TCG GTT AGG TTG	1584
Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Ser Val Arg Leu	
515 520 525	
CGG GCC TAC CTG AAC ACA CCA GGG TTG CCC GTT TGC CAG GAC CAC CTG	1632
Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu	
530 535 540	
GAG TTC TGG GAG AGT GTC TTC ACA GGC CTC ACC CAT ATA GAT GCA CAC	1680
Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His	
545 550 555 560	
TTC TTG TCC CAG ACC AAG CAG GCA GGA GAC AAC TTC CCC TAC CTG GTA	1728
Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val	
565 570 575	
GCA TAC CAA GCC ACG GTG TGC GCC AGG GCT CAG GCC CCA CCT CCA TCA	1776
Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser	
580 585 590	
TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA CCT ACG CTG CAC	1824
Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His	
595 600 605	
GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC CAA AAT GAG GTC	1872
Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Val	
610 615 620	
ACC CTC ACC CAC CCC ATA ACC AAA TAC ATC ATG GCA TGC ATG TCG GCC	1920
Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala	
625 630 635 640	
GAC CTG GAG GTC GTT ACG TAG	1941
Asp Leu Glu Val Val Thr	
645	

## (2) INFORMATION FOR SEQ ID NO:119:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1941 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1941

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

ATG CAT ATG CAT CAT CAT CAC CAT CAT CTG GTG CCG CGC GGC AGC GCG	48
---	----

186

Met	His	Met	His	His	His	His	His	His	His	Leu	Val	Pro	Arg	Gly	Ser	Ala	
1				5						10					15		
CCC	ATC	ACG	GCC	TAC	TCC	CAA	CAG	ACG	CGG	GGC	CTA	CTT	GGT	TGC	ATC		96
Pro	Ile	Thr	Ala	Tyr	Ser	Gln	Gln	Thr	Arg	Gly	Leu	Leu	Gly	Cys	Ile		
			20					25					30				
ATC	ACT	AGC	CTT	ACA	GGC	CGG	GAC	AAG	AAC	CAG	GTC	GAG	GGA	GAG	GTT		144
Ile	Thr	Ser	Leu	Thr	Gly	Arg	Asp	Lys	Asn	Gln	Val	Glu	Gly	Glu	Val		
		35					40					45					
CAG	GTG	GTT	TCC	ACC	GCA	ACA	CAA	TCC	TTC	CTG	GCG	ACC	TGC	GTC	AAC		192
Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala	Thr	Cys	Val	Asn		
	50					55					60						
GGC	GTG	TGT	TGG	ACC	GTT	TAC	CAT	GGT	GCT	GGC	TCA	AAG	ACC	TTA	GCC		240
Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser	Lys	Thr	Leu	Ala		
65					70				75						80		
GGC	CCA	AAG	GGG	CCA	ATC	ACC	CAG	ATG	TAC	ACT	AAT	GTG	GAC	CAG	GAC		288
Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	Val	Asp	Gln	Asp		
				85				90						95			
CTC	GTC	GGC	TGG	CAG	GCG	CCC	CCC	GGG	GCG	CGT	TCC	TTG	ACA	CCA	TGC		336
Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	Leu	Thr	Pro	Cys		
			100					105					110				
ACC	TGT	GGC	AGC	TCA	GAC	CTT	TAC	TTG	GTC	ACG	AGA	CAT	GCT	GAC	GTC		384
Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	His	Ala	Asp	Val		
		115					120					125					
ATT	CCG	GTG	CGC	CGG	CGG	GGC	GAC	AGT	AGG	GGG	AGC	CTG	CTC	TCC	CCC		432
Ile	Pro	Val	Arg	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	Leu	Leu	Ser	Pro		
	130					135						140					
AGG	CCT	GTC	TCC	TAC	TTG	AAG	GGC	TCT	TCG	GGT	GGT	CCA	CTG	CTC	TGC		480
Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly	Pro	Leu	Leu	Cys		
145					150					155					160		
CCT	TCG	GGG	CAC	GCT	GTG	GGC	ATC	TTC	CGG	GCT	GCC	GTA	TGC	ACC	CGG		528
Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	Val	Cys	Thr	Arg		
				165					170					175			
GGG	GTT	GCG	AAG	GCG	GTG	GAC	TTT	GTG	CCC	GTA	GAG	TCC	ATG	GAA	ACT		576
Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	Ser	Met	Glu	Thr		
			180					185					190				
ACT	ATG	CGG	TCT	CCG	GTC	TTC	ACG	GAC	AAC	TCA	TCC	CCC	CCG	GCC	GTA		624
Thr	Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser	Ser	Pro	Pro	Ala	Val		
		195					200					205					
CCG	CAG	TCA	TTT	CAA	GTG	GCC	CAC	CTA	CAC	GCT	CCC	ACT	GGC	AGC	GGC		672
Pro	Gln	Ser	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro	Thr	Gly	Ser	Gly		
	210					215					220						
AAG	AGT	ACT	AAA	GTG	CCG	GCT	GCA	TAT	GCA	GCC	CAA	GGG	TAC	AAG	GTG		720
Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	Gly	Tyr	Lys	Val		
225					230					235					240		

CTC	GTC	CTC	AAT	CCG	TCC	GTT	GCC	GCT	ACC	TTA	GGG	TTT	GGG	GCG	TAT	768
Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly	Phe	Gly	Ala	Tyr	
			245						250						255	
ATG	TCT	AAG	GCA	CAC	GGT	ATT	GAC	CCC	AAC	ATC	AGA	ACT	GGG	GTA	AGG	816
Met	Ser	Lys	Ala	His	Gly	Ile	Asp	Pro	Asn	Ile	Arg	Thr	Gly	Val	Arg	
			260					265					270			
ACC	ATT	ACC	ACA	GGC	GCC	CCC	GTC	ACA	TAC	TCT	ACC	TAT	GGC	AAG	TTT	864
Thr	Ile	Thr	Thr	Gly	Ala	Pro	Val	Thr	Tyr	Ser	Thr	Tyr	Gly	Lys	Phe	
		275					280						285			
CTT	GCC	GAT	GGT	GGT	TGC	TCT	GGG	GGC	GCT	TAT	GAC	ATC	ATA	ATA	TGT	912
Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	Ile	Ile	Ile	Cys	
	290					295					300					
GAT	GAG	TGC	CAT	TCA	ACT	GAC	TCG	ACT	ACA	ATC	TTG	GGC	ATC	GGC	ACA	960
Asp	Glu	Cys	His	Ser	Thr	Asp	Ser	Thr	Thr	Ile	Leu	Gly	Ile	Gly	Thr	
305					310					315					320	
GTC	CTG	GAC	CAA	GCG	GAG	ACG	GCT	GGA	GCG	CGG	CTT	GTC	GTG	CTC	GCC	1008
Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	Val	Val	Leu	Ala	
			325					330						335		
ACC	GCT	ACG	CCT	CCG	GGA	TCG	GTC	ACC	GTG	CCA	CAC	CCA	AAC	ATC	GAG	1056
Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Val	Pro	His	Pro	Asn	Ile	Glu	
			340					345					350			
GAG	GTG	GCC	CTG	TCT	AAT	ACT	GGA	GAG	ATC	CCC	TTC	TAT	GGC	AAA	GCC	1104
Glu	Val	Ala	Leu	Ser	Asn	Thr	Gly	Glu	Ile	Pro	Phe	Tyr	Gly	Lys	Ala	
	355						360					365				
ATC	CCC	ATT	GAA	GCC	ATC	AGG	GGG	GGA	AGG	CAT	CTC	ATT	TTC	TGT	CAT	1152
Ile	Pro	Ile	Glu	Ala	Ile	Arg	Gly	Gly	Arg	His	Leu	Ile	Phe	Cys	His	
	370					375					380					
TCC	AAG	AAG	AAG	TGC	GAC	GAG	CTC	GCC	GCA	AAG	CTG	TCA	GGC	CTC	GGA	1200
Ser	Lys	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Ala	Lys	Leu	Ser	Gly	Leu	Gly	
385				390						395					400	
ATC	AAC	GCT	GTG	GCG	TAT	TAC	CGG	GGG	CTC	GAT	GTG	TCC	GTC	ATA	CCA	1248
Ile	Asn	Ala	Val	Ala	Tyr	Tyr	Arg	Gly	Leu	Asp	Val	Ser	Val	Ile	Pro	
			405					410						415		
ACT	TCC	GGA	GAC	GTC	GTT	GTC	GTG	GCA	ACA	GAC	GCT	CTG	ATG	ACG	GGC	1296
Thr	Ser	Gly	Asp	Val	Val	Val	Val	Ala	Thr	Asp	Ala	Leu	Met	Thr	Gly	
			420					425					430			
TAT	ACG	GGC	GAC	TTT	GAC	TCA	GTG	ATC	GAC	TGT	AAC	ACA	TGT	GTC	ACC	1344
Tyr	Thr	Gly	Asp	Phe	Asp	Ser	Val	Ile	Asp	Cys	Asn	Thr	Cys	Val	Thr	
		435					440					445				
CAG	ACA	GTC	GAC	TTC	AGC	TTG	GAT	CCC	ACC	TTC	ACC	ATT	GAG	ACG	ACG	1392
Gln	Thr	Val	Asp	Phe	Ser	Leu	Asp	Pro	Thr	Phe	Thr	Ile	Glu	Thr	Thr	
	450					455					460					
ACC	GTG	CCT	CAA	GAC	GCA	GTG	TCG	CGC	TCG	CAG	CGG	CGG	GGT	AGG	ACT	1440

Thr	Val	Pro	Gln	Asp	Ala	Val	Ser	Arg	Ser	Gln	Arg	Arg	Gly	Arg	Thr		
465					470					475					480		
GGC	AGG	GGT	AGG	AGA	GGC	ATC	TAC	AGG	TTT	GTG	ACT	CCG	GGA	GAA	CGG	1488	
Gly	Arg	Gly	Arg	Arg	Gly	Ile	Tyr	Arg	Phe	Val	Thr	Pro	Gly	Glu	Arg		
				485					490					495			
CCC	TCG	GGC	ATG	TTC	GAT	TCC	TCG	GTC	CTG	TGT	GAG	TGC	TAT	GAC	GCG	1536	
Pro	Ser	Gly	Met	Phe	Asp	Ser	Ser	Val	Leu	Cys	Glu	Cys	Tyr	Asp	Ala		
			500					505						510			
GGC	TGT	GCT	TGG	TAC	GAG	CTC	ACC	CCC	GCC	GAG	ACC	TCG	GTT	AGG	TTG	1584	
Gly	Cys	Ala	Trp	Tyr	Glu	Leu	Thr	Pro	Ala	Glu	Thr	Ser	Val	Arg	Leu		
		515					520						525				
CGG	GCC	TAC	CTG	AAC	ACA	CCA	GGG	TTG	CCC	GTT	TGC	CAG	GAC	CAC	CTG	1632	
Arg	Ala	Tyr	Leu	Asn	Thr	Pro	Gly	Leu	Pro	Val	Cys	Gln	Asp	His	Leu		
		530				535						540					
GAG	TTC	TGG	GAG	AGT	GTC	TTC	ACA	GGC	CTC	ACC	CAT	ATA	GAT	GCA	CAC	1680	
Glu	Phe	Trp	Glu	Ser	Val	Phe	Thr	Gly	Leu	Thr	His	Ile	Asp	Ala	His		
545					550					555					560		
TTC	TTG	TCC	CAG	ACC	AAG	CAG	GCA	GGA	GAC	AAC	TTC	CCC	TAC	CTG	GTA	1728	
Phe	Leu	Ser	Gln	Thr	Lys	Gln	Ala	Gly	Asp	Asn	Phe	Pro	Tyr	Leu	Val		
				565					570					575			
GCA	TAC	CAA	GCC	ACG	GTG	TGC	GCC	AGG	GCT	CAG	GCC	CCA	CCT	CCA	TCA	1776	
Ala	Tyr	Gln	Ala	Thr	Val	Cys	Ala	Arg	Ala	Gln	Ala	Pro	Pro	Pro	Ser		
			580					585						590			
TGG	GAT	CAA	ATG	TGG	AAG	TGT	CTC	ATA	CGG	CTG	AAA	CCT	ACG	CTG	CAC	1824	
Trp	Asp	Gln	Met	Trp	Lys	Cys	Leu	Ile	Arg	Leu	Lys	Pro	Thr	Leu	His		
		595					600						605				
GGG	CCA	ACA	CCC	TTG	CTG	TAC	AGG	CTG	GGA	GCC	GTC	CAA	AAT	GAG	GTC	1872	
Gly	Pro	Thr	Pro	Leu	Leu	Tyr	Arg	Leu	Gly	Ala	Val	Gln	Asn	Glu	Val		
		610				615					620						
ACC	CTC	ACC	CAC	CCC	ATA	ACC	AAA	TAC	ATC	ATG	GCA	TGC	ATG	TCG	GCC	1920	
Thr	Leu	Thr	His	Pro	Ile	Thr	Lys	Tyr	Ile	Met	Ala	Cys	Met	Ser	Ala		
625					630					635					640		
GAC	CTG	GAG	GTC	GTT	ACG	TAG										1941	
Asp	Leu	Glu	Val	Val	Thr												
				645													

## (2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1941 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1941

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

ATG CAT ATG CAT CAT CAT CAC CAT CAT CTG GTG CCG CGC GGC AGC GCG	48
Met His Met His His His His His His Leu Val Pro Arg Gly Ser Ala	
1 5 10 15	
CCC ATC ACG GCC TAC TCC CAA CAG ACG CGG GGC CTA CTT GGT TGC ATC	96
Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly Cys Ile	
20 25 30	
ATC ACT AGC CTT ACA GGC CGG GAC AAG AAC CAG GTC GAG GGA GAG GTT	144
Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly Glu Val	
35 40 45	
CAG GTG GTT TCC ACC GCA ACA CAA TCC TTC CTG GCG ACC TGC GTC AAC	192
Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys Val Asn	
50 55 60	
GGC GTG TGT TGG ACC GTT TAC CAT GGT GCT GGC TCA AAG ACC TTA GCC	240
Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr Leu Ala	
65 70 75 80	
GGC CCA AAG GGG CCA ATC ACC CAG ATG TAC ACT AAT GTG GAC CAG GAC	288
Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp Gln Asp	
85 90 95	
CTC GTC GGC TGG CAG GCG CCC CCC GGG GCG CGT TCC TTG ACA CCA TGC	336
Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu Thr Pro Cys	
100 105 110	
ACC TGT GGC AGC TCA GAC CTT TAC TTG GTC ACG AGA CAT GCT GAC GTC	384
Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala Asp Val	
115 120 125	
ATT CCG GTG CGC CGG CGG GGC GAC AGT AGG GGG AGC CTG CTC TCC CCC	432
Ile Pro Val Arg Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu Ser Pro	
130 135 140	
AGG CCT GTC TCC TAC TTG AAG GGC TCT TCG GGT GGT CCA CTG CTC TGC	480
Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu Leu Cys	
145 150 155 160	
CCT TCG GGG CAC GCT GTG GGC ATC TTC CGG GCT GCC GTA TGC ACC CGG	528
Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys Thr Arg	
165 170 175	
GGG GTT GCG AAG GCG GTG GAC TTT GTG CCC GTG GAG TCC ATG GAA ACT	576
Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser Met Glu Thr	
180 185 190	

ACT	ATG	CGG	TCT	CCG	GTC	TTC	ACG	GAC	AAC	TCA	TCC	CCC	CCG	GCC	GTA	624
Thr	Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser	Ser	Pro	Pro	Ala	Val	
		195					200					205				
CCG	CAG	TCA	TTT	CAA	GTG	GCC	CAC	CTA	CAC	GCT	CCC	ACT	GGC	AGC	GGC	672
Pro	Gln	Ser	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro	Thr	Gly	Ser	Gly	
	210					215					220					
AAG	AGT	ACT	AAA	GTG	CCG	GCT	GCC	TAC	GCA	GCC	CAA	GGG	TAC	AAG	GTG	720
Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	Gly	Tyr	Lys	Val	
225					230					235					240	
CTC	GTC	CTC	AAT	CCG	TCC	GTT	GCC	GCT	ACC	TTA	GGG	TTT	GGG	GCG	TAT	768
Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly	Phe	Gly	Ala	Tyr	
			245						250					255		
ATG	TCT	AAG	GCA	CAC	GGT	ATT	GAC	CCC	AAC	ATC	AGA	ACT	GGG	GTA	AGG	816
Met	Ser	Lys	Ala	His	Gly	Ile	Asp	Pro	Asn	Ile	Arg	Thr	Gly	Val	Arg	
			260					265					270			
ACC	ATT	ACC	ACA	GGC	GCC	CCC	GTC	ACA	TAC	TCT	ACC	TAT	GGC	AAG	TTT	864
Thr	Ile	Thr	Thr	Gly	Ala	Pro	Val	Thr	Tyr	Ser	Thr	Tyr	Gly	Lys	Phe	
		275					280					285				
CTT	GCC	GAT	GGT	GGT	TGC	TCT	GGG	GGC	GCT	TAT	GAC	ATC	ATA	ATA	TGT	912
Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	Ile	Ile	Ile	Cys	
	290					295					300					
GAT	GAG	TGC	CAT	TCA	ACT	GAC	TCG	ACT	ACA	ATC	TTG	GGC	ATC	GGC	ACA	960
Asp	Glu	Cys	His	Ser	Thr	Asp	Ser	Thr	Thr	Ile	Leu	Gly	Ile	Gly	Thr	
305					310					315					320	
GTC	CTG	GAC	CAA	GCG	GAG	ACG	GCT	GGA	GCG	CGG	CTT	GTC	GTG	CTC	GCC	1008
Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	Val	Val	Leu	Ala	
			325					330						335		
ACC	GCT	ACG	CCT	CCG	GGA	TCG	GTC	ACC	GTG	CCA	CAC	CCA	AAC	ATC	GAG	1056
Thr	Ala	Thr	Pro	Pro	Gly	Ser	Val	Thr	Val	Pro	His	Pro	Asn	Ile	Glu	
			340					345					350			
GAG	GTG	GCC	CTG	TCT	AAT	ACT	GGA	GAG	ATC	CCC	TTC	TAT	GGC	AAA	GCC	1104
Glu	Val	Ala	Leu	Ser	Asn	Thr	Gly	Glu	Ile	Pro	Phe	Tyr	Gly	Lys	Ala	
		355				360						365				
ATC	CCC	ATT	GAA	GCC	ATC	AGG	GGG	GGA	AGG	CAT	CTC	ATT	TTC	TGT	CAT	1152
Ile	Pro	Ile	Glu	Ala	Ile	Arg	Gly	Gly	Arg	His	Leu	Ile	Phe	Cys	His	
	370					375					380					
TCC	AAG	AAG	AAG	TGC	GAC	GAG	CTC	GCC	GCA	AAG	CTG	TCA	GGC	CTC	GGA	1200
Ser	Lys	Lys	Lys	Cys	Asp	Glu	Leu	Ala	Ala	Lys	Leu	Ser	Gly	Leu	Gly	
385					390					395					400	
ATC	AAC	GCT	GTG	GCG	TAT	TAC	CGG	GGG	CTC	GAT	GTG	TCC	GTC	ATA	CCA	1248
Ile	Asn	Ala	Val	Ala	Tyr	Tyr	Arg	Gly	Leu	Asp	Val	Ser	Val	Ile	Pro	
				405				410						415		
ACT	ATC	GGA	GAC	GTC	GTT	GTC	GTG	GCA	ACA	GAC	GCT	CTG	ATG	ACG	GGC	1296
Thr	Ile	Gly	Asp	Val	Val	Val	Val	Ala	Thr	Asp	Ala	Leu	Met	Thr	Gly	



420	425	430	
TAT ACG GGC GAC TTT GAC TCA GTG ATC GAC TGT AAC ACA TGT GTC ACC Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys Val Thr 435 440 445			1344
CAG ACA GTC GAC TTC AGC TTG GAT CCC ACC TTC ACC ATT GAG ACG ACG Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu Thr Thr 450 455 460			1392
ACC GTG CCT CAA GAC GCA GTG TCG CGC TCG CAG CGG CGG GGT AGG ACT Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly Arg Thr 465 470 475 480			1440
GGC AGG GGT AGG AGA GGC ATC TAC AGG TTT GTG ACT CCG GGA GAA CGG Gly Arg Gly Arg Arg Gly Ile Tyr Arg Phe Val Thr Pro Gly Glu Arg 485 490 495			1488
CCC TCG GGC ATG TTC GAT TCC TCG GTC CTG TGT GAG TGC TAT GAC GCG Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr Asp Ala 500 505 510			1536
GGC TGT GCT TGG TAC GAG CTC ACC CCC GCC GAG ACC TCG GTT AGG TTG Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Ser Val Arg Leu 515 520 525			1584
CGG GCC TAC CTG AAC ACA CCA GGG TTG CCC GTT TGC CAG GAC CAC CTG Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu 530 535 540			1632
GAG TTC TGG GAG AGT GTC TTC ACA GGC CTC ACC CAT ATA GAT GCA CAC Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp Ala His 545 550 555 560			1680
TTC TTG TCC CAG ACC AAG CAG GCA GGA GAC AAC TTC CCC TAC CTG GTA Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr Leu Val 565 570 575			1728
GCA TAC CAA GCC ACG GTG TGC GCC AGG GCT CAG GCC CCA CCT CCA TCA Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro Pro Ser 580 585 590			1776
TGG GAT CAA ATG TGG AAG TGT CTC ATA CGG CTG AAA CCT ACG CTG CAC Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr Leu His 595 600 605			1824
GGG CCA ACA CCC TTG CTG TAC AGG CTG GGA GCC GTC CAA AAT GAG GTC Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn Glu Val 610 615 620			1872
ACC CTC ACC CAC CCC ATA ACC AAA TAC ATC ATG GCA TGC ATG TCG GCC Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met Ser Ala 625 630 635 640			1920
GAC CTG GAG GTC GTT ACG TAG Asp Leu Glu Val Val Thr 645			1941

## (2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 36 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GCUCGCCCCGG GGAUCCUCUA GGAUACACG UUCGAU 36

## (2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 36 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

CUAGAGGAUC CCCGGGCGAG CCCUAUAGUG AGUCGU 36

## (2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 21 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GCTCGCCCCGG GGATCCTCTA G 21